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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
An. Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, author, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 = 703-308-4498
ian.delaval@uspto.gov

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Searcher	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	SA: Sequence (#) _____	STN _____
Searcher: Phone # <u>4498</u>	AA: Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher: Location _____	Structure (#) _____	Questel Orbit _____
Date: Requester: <u>12/12</u>	Bibliographic _____	Dr. Link _____
Date: Completed: <u>12/12</u>	Litigation _____	Lexis Nexis _____
Searcher: Prep & Review Time _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Client: Prep Time <u>15</u>	Patent Family _____	WWW Internet _____
Other: <u>#10</u>	Other _____	Other (specify) _____



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 109419

TO: Phillip Gambel
Location: 8b13 / 9e12
Tuesday, December 02, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 772103

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

STIC
09/12/03
Biotech-Chem Library
09/12/03
jan.delaval@uspto.gov

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:39:15; Search time 15.8316 Seconds

(without alignments)
1354.605 Million cell updates/sec

Title: US-09-772-103-2

Sequence: 1174

Sequence: 1 MACLGFORHKAQNLATRTW.....MPPTPECEKQFPYFIPIN 223

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR 76: *
2: PIR: *
3: PIR: *
4: PIR: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1159	98.7	223	2	cytotoxic T-lympho
2	997	84.9	223	2	CTLA-4 precursor
3	970	82.6	186	2	cytotoxic T-lympho
4	878	74.8	223	2	cytotoxic T-lympho
5	211	18.0	221	2	CD28 protein - ch
6	204	17.4	221	2	CD28 precursor - r
7	200	17.0	36	2	cytotoxic T-lympho
8	187	15.9	220	1	CD28 precursor - r
9	174.5	14.9	173	2	cytotoxic T-lympho
10	170	14.5	218	2	cell surface gly
11	158	13.5	218	2	cell surface gly
12	101	8.6	132	2	cell surface gly
13	100.5	8.6	132	2	cell surface gly
14	99	8.4	124	2	cell surface gly
15	97	8.3	108	2	cell surface gly
16	97	8.3	108	2	cell surface gly
17	94	8.0	117	2	cell surface gly
18	93	7.9	117	2	cell surface gly
19	92	7.8	117	2	cell surface gly
20	91	7.8	108	2	cell surface gly
21	91	7.8	108	2	cell surface gly
22	90.5	7.7	108	2	cell surface gly
23	90.5	7.7	123	2	cell surface gly
24	90	7.7	140	2	cell surface gly
25	89.5	7.6	3707	2	cell surface gly
26	89	7.6	125	2	cell surface gly
27	88	7.5	573	2	cell surface gly
28	87.5	7.5	88	2	cell surface gly
29	87.5	7.5	213	2	cell surface gly

30	87	7.4	207	2	150609	T-cell surface gly
31	87	7.4	739	2	JS0675	vascular cell adhe
32	86	7.3	120	2	S30525	ig lambda chain v
33	86	7.3	125	2	S40349	ig kappa chain v-j
34	86	7.3	199	2	S78540	inducible t-cell c
35	86	7.3	224	2	S14237	ig kappa chain pre
36	86	7.3	739	2	UN0581	vascular cell adhe
37	85.5	7.3	598	2	T42070	protein serine/thr
38	85	7.2	111	2	S36281	ig lambda chain v
39	85	7.2	112	2	PL0274	ig kappa chain v r
40	85	7.2	125	2	S40333	ig kappa chain v-j
41	85	7.2	1367	2	A41228	protein-tyrosine k
42	84.5	7.2	105	2	S26338	ig kappa chain v r
43	84.5	7.2	124	2	S40318	ig kappa chain v r
44	84	7.2	111	2	S38497	ig lambda chain -
45	84	7.2	112	2	H26317	ig kappa chain v r

ALIGNMENTS

RESULT 1
T09536
cytotoxic T-lymphocyte protein 4 - human
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C/Accession: T09536
J/Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
R/Immunol. 147, 1037-1044, 1991
A/Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mo
A/Reference number: 149584; MUID:91318145; PMID:1713603
A/Accession: T09536
A/Status: preliminary; translated from GB/EMBL/DBDUT
A/Molecule type: mRNA
A/Residues: 1-223 <HAR>
A/Cross-references: EMBL:L15006; NID:g291928; PIDN:AAB59385.1; PID:g291929
C/Genetics:
A/Map position: 2q33
C/Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C/Keywords: T-cell; transmembrane protein

Query Match 98.7%; Score 1159; DB 2; Length 223;
Best Local Similarity 98.7%; Pred. No. 7.2e-100;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWCTLLFFLLFVPCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWCTLLFFLLFVPCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASBGRATEVRVTLRQADSOVTEVCATYTMGNELTFDDSICTGSSGNQNLITQGR 120
DB 61 ASBGRATEVRVTLRQADSOVTEVCATYTMGNELTFDDSICTGSSGNQNLITQGR 120
QY 121 AMDTGLYICKVLMAMPYLYLIGNGAQIYVIDPECPDSDFLMLAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVLMAMPYLYLIGNGAQIYVIDPECPDSDFLMLAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPPTPECEKQFPYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPPTPECEKQFPYFIPIN 223

RESULT 2

I46696

CTLA-4 precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C/Accession: I46696
R/Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A/Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecu
A/Reference number: I46689; MUID:95369849; PMID:7642234

A:Accession: 146696
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-223 <ISO>
 A:Cross-references: GB:049844; NID:g755100; PIDN:BA08644.1; PID:g755101
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

Query Match 84.9%; Score 997; DB 2; Length 223;
 Best Local Similarity 84.3%; Pred. No. 7, 1e-85;
 Matches 188; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCITLFLFIPVCKAMHVAQPAVLAASRGIAFPVCEY 60
 DB 1 MARLGFQROCTQDLASRTWSCALFSLFLPVSFKLHVSQPAVLAASRGVAFVCEY 60
 QY 61 ASGKATEVAVTVLRQADSOVTEVCATVMKGNELFLDLSICTGSSGNQVNLTIQGR 120
 DB 61 ASHKAIEVAVTVLRQANSQTEVCATVVENELTFIDSTCTGISHKRVNLTIQGLS 120
 QY 121 AMDTGLYICKVELMPPPYVIGNGAQIYVIDPEPCPSDPLMLIAAVSGLFFYSFL 180
 DB 121 AMDTGLYICKVELMPPPYVIGMNGQIYVIEBPDPDPLMLIAAISGLFFYSFL 180
 QY 181 LTAVALSKMLKKRSPLTGGVYVKKMPTEPCCKQOPFYFIPIN 223
 DB 181 ITAVLSLKMKKRSPLTGGVYVKKMPTEPCCKQOPFYFIPIN 223

RESULT 3

S08614
 cytotoxic T-lymphocyte protein 4 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
 C:Accession: S08614
 R:Darivach, P.; Mattei, M.G.; Golstein, P.; Lefranc, M.P.
 Eur. J. Immunol. 18, 1901-1905, 1988
 A:title: Human Ig superfamily CTLA-4 gene: chromosomal localization and identity of prod
 A:Reference number: S08614; MUID:89120925; PMID:3220103
 A:Accession: S08614
 A:Molecule type: DNA
 A:Residues: 1-186 <DAR>
 A:Cross-references: EMBL:X15070; NID:g30283; PID:g825649
 C:Genetics:
 A:Gene: GDB:CTLA4
 A:Cross-references: GDB:119818; OMIM:123890
 A:Map position: 2q33-2q33
 A:Introns: 116/1; 152/3
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein
 F:125-150/Domain: transmembrane #status predicted <TMM>
 F:151-186/Domain: intracellular #status predicted <INT>
 F:21-92/Disulfide bonds: #status predicted

Query Match 82.6%; Score 970; DB 2; Length 186;
 Best Local Similarity 100.0%; Pred. No. 1, 8e-82;
 Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 MHVAQPAVLAASRGIAFPVCEYASRGKATEVAVTVLRQADSOVTEVCATVMKGNELTF 97
 DB 1 MHVAQPAVLAASRGIAFPVCEYASRGKATEVAVTVLRQADSOVTEVCATVMKGNELTF 60
 QY 98 LDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYVIGNGAQIYVIDPEPC 157
 DB 61 LDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPYVIGNGAQIYVIDPEPC 120
 QY 158 PDSDFLMLIAAVSGLFFYSFLITAVLSLKMKKRSPLTGGVYVKKMPTEPCCKQOP 217
 DB 121 PDSDFLMLIAAVSGLFFYSFLITAVLSLKMKKRSPLTGGVYVKKMPTEPCCKQOP 180
 QY 218 YFIPIN 223
 DB 181 YFIPIN 186

RESULT 4

A29063
 cytotoxic T-lymphocyte protein 4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 05-Nov-1999
 C:Accession: A29063; 149622
 R:Brinnet, J.F.; Denizot, F.; Luciani, M.F.; Roux-Dosseto, M.; Suzan, M.; Mattei, M.G.;
 Nature 328, 267-270, 1987
 A:title: A new member of the immunoglobulin superfamily--CTLA-4.
 A:Reference number: A29063; MUID:87258259; PMID:3496540
 A:Accession: A29063
 A:Molecule type: mRNA
 A:Residues: 1-223 <BRU>
 A:Cross-references: GB:X05719; NID:g50592; PIDN:CAA29191.1; PID:g50593
 R:Harper, K.; Balzano, C.; Kourlier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
 J. Immunol. 147, 1037-1044, 1991
 A:title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mou
 A:Reference number: 149584; MUID:91318145; PMID:1713603
 A:Accession: 149622
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-36 <RES>
 A:Cross-references: GB:M74362; NID:g192833; PIDN:AAA7489.1; PID:g553903
 C:Genetics:
 A:Gene: CTLA-4
 A:Map position: 1, band C
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein

Query Match 74.8%; Score 878; DB 2; Length 223;
 Best Local Similarity 74.0%; Pred. No. 7, 4e-74;
 Matches 185; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCITLFLFIPVCKAMHVAQPAVLAASRGIAFPVCEY 60
 DB 1 MACLGFORHKAQNLATRTWPCITLFLFIPVCEAIDQVQPSVLAASHGVAFVCEY 60
 QY 61 ASGKATEVAVTVLRQADSOVTEVCATVMKGNELFLDLSICTGSSGNQVNLTIQGR 120
 DB 61 SPSHNTDEVAVTVLRQNDQMTVCATTFTEKNTGTFIDLPSCGTFVBSRVNLTIQGR 120
 QY 121 AMDTGLYICKVELMPPPYVIGNGAQIYVIDPEPCPSDPLMLIAAVSGLFFYSFL 180
 DB 121 AMDTGLYICKVELMPPPYVIGMNGQIYVIDPEPCPSDPLMLIAAVSGLFFYSFL 180
 QY 181 LTAVALSKMLKKRSPLTGGVYVKKMPTEPCCKQOPFYFIPIN 223
 DB 181 VSAVLSLKMKKRSPLTGGVYVKKMPTEPCCKQOPFYFIPIN 223

RESULT 5

S25168
 CHT28 protein - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: I50619; S25168
 R:Young, J.R.; Davidson, T.F.; Tregaskes, C.A.; Rennie, M.C.; Vainio, O.
 J. Immunol. 152, 3848-3851, 1994
 A:title: Monomeric homologue of mammalian CD28 is expressed on chicken T cells.
 A:Reference number: I50619; MUID:94194147; PMID:8144954
 A:Accession: I50619
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-221 <YO2>
 A:Cross-references: EMBL:X67915; NID:g63221; PIDN:CAA48114.1; PID:g63222
 C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
 C:Keywords: transmembrane protein

Query Match 18.0%; Score 211; DB 2; Length 221;
 Best Local Similarity 31.5%; Pred. No. 4, 1e-12;
 Matches 67; Conservative 36; Mismatches 88; Indels 22; Gaps 10;

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:49 ; Search time 10.4037 Seconds
(without alignments)
1008.007 Million cell updates/sec

Title: US-09-772-103-2
Perfect score: 1174
Sequence: 1 NACLGFQRHKAQLNLTATRTM.....MPPTRECEKQRPYFIPIN 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1170	99.7	223	1	CTLA4_HUMAN
2	1010	86.0	223	1	CTLA4_PIG
3	997	84.9	223	1	CTLA4_RABIT
4	878	74.8	223	1	CTLA4_MOUSE
5	211	18.0	221	1	CD28_CHICK
6	204	17.4	221	1	CD28_BOVIN
7	203	17.3	219	1	CD28_HUMAN
8	187	15.9	220	1	CD28_MOUSE
9	170	14.5	218	1	CD28_MOUSE
10	156	13.3	218	1	CD28_MOUSE
11	93	7.9	301	1	NADA_CLOPE
12	91	7.8	4391	1	PGEM_HUMAN
13	89.5	7.6	3707	1	PGEM_MOUSE
14	87	7.4	739	1	VCAI_RAT
15	86	7.3	739	1	VCAI_MOUSE
16	85	7.2	1356	1	VGR2_HUMAN
17	85	7.2	1367	1	VGR2_MOUSE
18	84	7.2	480	1	SAHH_XANPC
19	83	7.1	111	1	LV2D_HUMAN
20	83	7.1	111	1	LV2D_HUMAN
21	83	7.1	1343	1	VGR2_RAT
22	82	7.0	215	1	CTB2_HUMAN
23	81.5	6.9	111	1	KV12_RABIT
24	81.5	6.9	1897	1	PTPF_HUMAN
25	81	6.9	246	1	MOG_MOUSE
26	80.5	6.9	568	1	PHAC_CHRYO
27	80.5	6.9	715	1	LOC1_LACIA
28	79.5	6.8	108	1	KV6K_MOUSE
29	79	6.7	550	1	Q9JIB8_MOUSE
30	79	6.7	552	1	Q9JIB8_MOUSE
31	78.5	6.7	108	1	VGLF_HSVEL
32	78.5	6.7	145	1	KV1H_HUMAN
33	78	6.6	480	1	SAHH_XANPC

ALIGNMENTS

34	78	6.6	480	1	SAHH_XYLPA	O9pej1 xylella fas
35	78	6.6	485	1	SAHH_MESCR	P93253 mesembryant
36	78	6.6	3038	1	TRIO_HUMAN	O75962 homo sapien
37	77.5	6.6	226	1	CT9A_HUMAN	P11912 homo sapien
38	77.5	6.6	345	1	OPCM_BOVIN	P11834 bos taurus
39	77.5	6.6	345	1	OPCM_HUMAN	O14982 homo sapien
40	77	6.6	109	1	KV01_RAT	P01681 rattus norv
41	76.5	6.5	129	1	KV3M_HUMAN	P18136 homo sapien
42	76.5	6.5	466	1	SAHH_BRUME	O9ye49 bruceilla me
43	76.5	6.5	1203	1	PTC2_HUMAN	O9y6c5 homo sapien
44	76	6.5	109	1	LV2E_HUMAN	P01708 homo sapien
45	76	6.5	114	1	KV4A_HUMAN	P01625 homo sapien

RESULT 1

ID	CTLA4_HUMAN	STANDARD;	PRT;	223 AA.
AC	P16410; Q8WKJ1; Q96P43; Q9UKN9;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Cytotoxic T-lymphocyte protein 4 precursor (Cytotoxic T-lymphocyte-associated antigen 4) (CTLA-4) (CD152 antigen).			
GN	CTLA4 OR CD152.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21601151; PubMed=11735222;			
RA	Ling V., Wu P.W., Flinterly H.F., Agostino M.J., Graham J.R., Chen S.,			
RT	Justiff J., Fisk G.J., Miller C.P., Collins M.;			
RT	"Assembly and annotation of human chromosome 2q33 sequence containing			
RT	the CD28, CTLA4, and ICOS gene cluster: analysis by computational,			
RT	comparative, and microarray approaches.";			
RL	Genomics 78:155-168(2001).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91318145; PubMed=1713603;			
RA	Harper K., Balzano C., Rouvier E., Mattei M.-G., Luciani M.F.,			
RT	Goistein P.;			
RT	"CTLA-4 and CD28 activated lymphocyte molecules are closely related			
RT	in both mouse and human as to sequence, message expression, gene			
RT	structure, and chromosomal location.";			
RL	J. Immunol. 147:1037-1044(1991).			
RN	(4)			
RP	SEQUENCE OF 38-223 FROM N.A.			
RX	TISSUE=Lymphocytes;			
RC	MEDLINE=89120925; PubMed=3220103;			
RA	Dattavach P., Mattei M.-G., Goistein P., Lefranc M.-P.;			
RT	"Human Ig superfamily CTLA-4 gene: chromosomal localization and			
RT	identity of protein sequence between murine and human CTLA-4			
RT	cytoplasmic domains.";			
RL	Eur. J. Immunol. 18:1901-1905(1988).			
RN	(5)			
RP	SEQUENCE OF 140-223 FROM N.A., AND TISSUE SPECIFICITY.			
RX	MEDLINE=99425274; PubMed=10493833;			
RA	Ling V., Wu P.W., Flinterly H.F., Sharpe A.H., Gray G.S., Collins M.;			
RT	"Complete sequence determination of the mouse and human CTLA4 gene			
RT	loci: cross-species DNA sequence similarity beyond exon borders.";			
RL	Genomics 60:341-355(1999).			
RN	(6)			
RP	FUNCTION.			
RX	MEDLINE=91341416; PubMed=1714933;			

RA Linsley P.S., Brady W., Urnes M., Griesmaire L.S., Dangle N.K.,
 RA Ledbetter J.A.;
 RT "CTLA-4 is a second receptor for the B cell activation antigen B7.";
 RL J. Exp. Med. 174:561-569(1991).
 RN [17]
 RP STRUCTURE BY NMR OF 37-165.
 RX MEDLINE=97372889; PubMed=9228944;
 RA Metzler W.J., Bajorath U., Fenderson W., Shaw S.Y., Constantine K.L.,
 RA Naemura P.S.;
 RA Linsley P.S.;
 RT "Solution structure of human CTLA-4 and delineation of a CD80/CD86
 RT binding site conserved in CD28.";
 RL Nat. Struct. Biol. 4:527-531(1997).
 RN [18]
 RP VARIANT ALA-17, AND ASSOCIATION WITH IDDM12.
 RX MEDLINE=97402209; PubMed=9259273;
 RA Maron M.P., Raffel L.J., Garchon H.-J., Jacob C.O., Serrano-Rios M.,
 RA Martinez Larad M.T., Teng W.-P., Park Y., Zhang Z.-X.,
 RA Goldstein D.R., Tao Y.-W., Beaurain G., Bach J.-F., Huang H.-S.,
 RA Luo D.-F., Zeidler A., Rotter J.I., Yang M.C.K., Modilevsky T.,
 RA MacLaren N.K., She J.-X.;
 RT "Insulin-dependent diabetes mellitus (IDDM) is associated with CTLA4
 RT polymorphisms in multiple ethnic groups.";
 RL Hum. Mol. Genet. 6:1275-1282(1997).
 RN [19]
 RP POLYMORPHISM, AND ASSOCIATION WITH COELIAC DISEASE.
 RX MEDLINE=9205840; PubMed=10189842;
 RA Djilali-Saiah I., Schmitz J., Harfouch-Hamoud E., Mougnot J.-F.,
 RA Bach J.-F., Galliat-Zucman S.;
 RT "CTLA-4 gene polymorphism is associated with predisposition to coeliac
 RT disease.";
 RL Gut 43:187-189(1998).
 RN [10]
 RP VARIANT ALA-17, AND ASSOCIATION WITH TAO.
 RX MEDLINE=99402177; PubMed=10475192;
 RA Vaidya B., Imrie H., Petros P., Dickinson J., McCarthy M.I.,
 RA Kendall-Taylor P., Pearce S.H.S.;
 RT "Cytotoxic T lymphocyte antigen-4 (CTLA-4) gene polymorphism confers
 RT susceptibility to thyroid associated orbitopathy.";
 RL Lancet 354:743-744(1999).
 RN [11]
 RP VARIANT ALA-17, AND ASSOCIATION WITH GRD.
 RX MEDLINE=20385252; PubMed=10924276;
 RA Chistyakov D.A., Savost'yanov K.V., Turakulov R.I., Petunina N.A.,
 RA Trukhina L.V., Kudimova A.V., Balabolkin M.I., Nosikov V.V.;
 RT "Complex association analysis of Graves disease using a set of
 RT polymorphic markers.";
 RL Mol. Genet. Metab. 70:214-218(2000).
 RN [12]
 RP VARIANT ALA-17.
 RX MEDLINE=20395844; PubMed=10903931;
 RA Deng Z., Morse J.H., Slager S.L., Cuervo N., Moore K.J., Venetos G.,
 RA Kalachikov S., Cayanis E., Fischer S.G., Barst R.J., Hodge S.B.,
 RA Knowles J.A.;
 RT "Familial primary pulmonary hypertension (gene PPH1) is caused by
 RT mutations in the bone morphogenetic protein receptor-II gene.";
 RL Am. J. Hum. Genet. 67:737-744(2000).
 CC -1- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1
 CC (CD80) AND B7-2 (CD86).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in
 CC lymphoid tissues.
 CC -1- POLYMORPHISM: The variant Ala-17 is associated with an increased
 CC risk for autoimmune disorders as Graves disease (GRD), type I
 CC insulin-dependent diabetes mellitus (IDDM12), and thyroid-
 CC associated orbitopathy (TAO). The variant Thr-17 is associated
 CC with predisposition to coeliac disease, a gluten sensitive
 CC enteropathy characterized by small bowel mucosal atrophy.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD152 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd152.htm".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF411058; AAL40932.1; -;
 DR EMBL; AF414120; AAL07473.1; -;
 DR EMBL; M74363; AAA52127.1; -;
 DR EMBL; M37245; AAA52773.1; -;
 DR EMBL; M37243; AAA52773.1; JOINED.
 DR EMBL; M37244; AAA52773.1; JOINED.
 DR EMBL; AF142144; AAF02499.1; -;
 DR PIR; S08614; S08614.
 DR PDB; 1AH1; 15-APR-98.
 DR PDB; 1HE6; 28-NOV-01.
 DR PDB; 1I85; 04-APR-01.
 DR PDB; 1I8L; 04-APR-01.
 DR Genew; HGNC:2505; CTLA4.
 DR MIM; 123890; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; FALSE NEG.
 KW Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal;
 KW 3d-structure; Polymorphism.
 FT SIGNAL 1 35
 FT CHAIN 36 223
 FT DOMAIN 36 161
 FT TRANSMEM 162 187
 FT DOMAIN 188 223
 FT DOMAIN 39 140
 FT DISULFID 58 129
 FT DISULFID 85 103
 FT CARBOHYD 113 113
 FT VARIANT 17 17
 FT FT
 FT CONFLICT 147 147
 FT STRAND 45 47
 FT TURN 50 51
 FT STRAND 53 59
 FT STRAND 70 76
 FT STRAND 81 88
 FT TURN 91 92
 FT TURN 99 100
 FT STRAND 104 108
 FT TURN 109 110
 FT STRAND 111 117
 FT TURN 121 123
 FT STRAND 125 132
 FT TURN 137 138
 FT STRAND 142 143
 FT STRAND 147 150
 SQ SEQUENCE 223 AA; 24656 MW; 6F9466FB2E139A5A CRC64;
 Query Match 99.7%; Score 1170; DB 1; Length 223;
 Best Local Similarity 99.6%; Pred. No. 1,3e-99;
 Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 MACLGFOHKAQNLNATRPCTLLFFLLPVPCKAMHVAQPAVLAASRGISPVCEY 60
 Db 1 MACLGFOHKAQNLNATRPCTLLFFLLPVPCKAMHVAQPAVLAASRGISPVCEY 60
 Oy 61 ASPKATEVRVTVLRQADSQVTEVCATYMMGNELTFLDLSICTGTSNGQVNLTIQGLR 120
 Db 61 ASPKATEVRVTVLRQADSQVTEVCATYMMGNELTFLDLSICTGTSNGQVNLTIQGLR 120
 Oy 121 AMDGLYICKEILMVPPTYYIGNGAQIYVIDEPCPSDFLLMILAANSSGLFFYSFL 180
 Db 121 AMDGLYICKEILMVPPTYYIGNGAQIYVIDEPCPSDFLLMILAANSSGLFFYSFL 180

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:33:29 ; Search time 37.9959 Seconds

(Without alignments)
1514.523 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGFORHKAQLNATRTM.....MPTPECKRQFPYPIPLN 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_archaea:*
2: SP_bacteria:*
3: SP_fungi:*
4: SP_human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP Vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1122	95.6	223	6	Q9BDN7	Q9bdn7 papio anubi
2	1118	95.2	223	6	Q9BDN7	Q9bdn7 papio anubi
3	1076	91.7	223	6	Q9BDP1	Q9bdp1 aotus crivi
4	1034	88.1	223	6	Q9XTA1	Q9xta1 felis silve
5	1032	87.9	223	6	Q9XTA1	Q9xta1 felis silve
6	1022	87.1	223	6	Q9GKP2	Q9gkp2 canis faml
7	1014	86.4	223	6	Q9GKP2	Q9gkp2 canis faml
8	1006	85.7	223	6	Q9N186	Q9n186 sus scrofa
9	997	84.9	223	6	Q9XSI1	Q9xsi1 canis faml
10	996	84.8	223	11	Q9JLV3	Q9jlv3 marmota mon
11	984	83.8	221	6	Q28090	Q28090 bos taurus
12	975	83.0	221	6	Q97631	Q97631 ovis aries
13	896	76.3	223	11	Q62859	Q62859 rattus norv
14	842	71.7	160	4	Q8TDA6	Q8tda6 homo sapien
15	592	50.4	137	4	Q95653	Q95653 homo sapien
16	587	50.0	115	4	Q9BZK2	Q9bzK2 homo sapien

17	534	45.5	174	11	Q9Z1A7	Q9z1a7 rattus norv
18	302	25.7	102	11	Q8CH94	Q8ch94 mus musculus
19	252	21.5	68	11	Q99PP8	Q99pf8 cricetus
20	199.5	17.0	221	6	Q9GKP3	Q9gkp3 canis faml
21	198	16.9	219	6	Q97630	Q97630 ovis aries
22	196.5	16.7	221	6	Q9N0N8	Q9n0n8 canis faml
23	191.5	16.3	221	6	Q02757	Q02757 felis silve
24	190.5	16.2	221	6	Q9N214	Q9n214 felis silve
25	189	16.1	220	6	Q9BDN2	Q9bdn2 callithrix
26	188.5	16.1	220	6	Q9BDN8	Q9bdn8 papio anubi
27	187.5	16.0	220	6	Q9BDM8	Q9bdm8 macaca neme
28	186.5	15.9	220	6	Q9BDN5	Q9bdn5 macaca neme
29	185.5	15.8	221	11	Q9JLV4	Q9jlv4 marmota mon
30	179	15.2	218	11	Q8CDB3	Q8cdB3 mus musculus
31	178.5	15.2	220	6	Q9BDM6	Q9bdm6 macaca mula
32	174.5	14.9	173	6	Q28289	Q28289 canis faml
33	128.5	10.9	138	6	Q8HYR9	Q8hyr9 bos taurus
34	113.5	9.7	201	4	Q14931	Q14931 homo sapien
35	112	9.5	176	6	Q95UB8	Q95jb8 macaca fasc
36	110.5	9.4	192	11	Q8CFD9	Q8cfD9 rattus norv
37	110	9.4	176	4	Q95667	Q95667 homo sapien
38	109	9.3	180	6	Q8MJ02	Q8mj02 macaca mula
39	108.5	9.2	192	11	Q8CG11	Q8cg11 rattus norv
40	108	9.2	144	11	Q9Z1A8	Q9z1a8 mus musculus
41	107	9.1	177	4	Q14930	Q14930 homo sapien
42	107	9.1	190	4	Q14932	Q14932 homo sapien
43	106.5	9.1	151	6	Q8MJ01	Q8mj01 macaca mula
44	103.5	8.8	152	4	Q95668	Q95668 homo sapien
45	103.5	8.8	165	4	Q95669	Q95669 homo sapien

ALIGNMENTS

RESULT 1

Q9BDN7 ID Q9BDN7 PRELIMINARY; PRT; 223 AA.
AC Q9BDN7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CD152 protein precursor.
GN CTA-4.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9595;
RN [1]
RP MEDLINE=21383618; PubMed=11491535;
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344838; AAK37534.1; -
DR HSSP; P16410; IAH1.
DR InterPro; IPR003596; IG-V.
DR SMART; SM00406; IGV; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 223 AA; 24655 MW; EC18C279CCCS666 CRC64;

Query Match 95.6%; Score 1122; DB 6; Length 223;
Best Local Similarity 96.9%; Pred. No. 8.4e-106;

Matches 216; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQLNATRTMPCCTLLFLLFPIPVCKAMHVAQPAVLAASSRGISFVCEY 60
DB 1 MACLGFORHKAQLNATRTMPCCTLLFLLFPIPVCKAMHVAQPAVLAASSRGISFVCEY 60
QY 61 ASPKATEVRVTVLRQDSQVTEVCAATYMMGNELTFLEDSICTGTSSGNQVNLTIQCLR 120

Db 61 ASFGKATEVAVYLRQADSOVTEVCAATYMGNELTFLDLSICTGSSGNQVNLITIGLR 120
 QY 121 AMDTGILYICKVELMPPPYLYGIGNGAQIYVIDPEPCDPSDFLMTAAVSSGLFFYSFL 180
 Db 121 AMDTGILYICKVELMPPPYLYGIGNGAQIYVIDPEPCDPSDFLMTAAVSSGLFFYSFL 180
 QY 181 LTAVALSKMLKKRSPITTGYYVKNPPTPECECKQFOPIPIPN 223
 Db 181 LTAVALSKMLKKRSPITTGYYVKNPPTPECECKQFOPIPIPN 223

RESULT 2

Q9BDC4 PRELIMINARY; PRT; 223 AA.
 ID Q9BDC4;
 AC Q9BDC4;
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE CD152 protein precursor.
 GN CTLA-4.
 OS Macaca mulatta (Rhesus macaque).
 OS Macaca nemestrina (Pig-tailed macaque), and
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NCBI_TaxID=9544, 9545, 9531;
 [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta, M.nemestrina, and C.torquatus atys;
 RA Villinger F., Boeslik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing and homology analysis of nonhuman primate
 RT Fas/Fas-Ligand and co-stimulatory molecules.";
 RL Immunogenetics 0:0-0(2001).
 DR EMBL; AF344846; AAK37605.1; -;
 DR EMBL; AF344854; AAK37537.1; -;
 DR EMBL; AF344848; AAK37608.1; -;
 DR HSSP; P16410; 1AH1.
 DR InterPro: IPR003596; IG_V.
 DR SMART; SM00406; IG; 1.
 KW SIGNAL.
 FT SIGNAL.
 FT VARIANT 223 223 N -> D.
 SQ SEQUENCE 223 AA; 24683 MW; BDE4248A00398FA CRC64;

Query Match 95.2%; Score 1118; DB 6; Length 223;
 Best Local Similarity 96.4%; Pred. No. 2.1e-105;
 Matches 215; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQDLATRTWPCITLFFLLFIPVFCAMHVAQPAVAVLASSRGIAAFVCEY 60
 Db 1 MACLGFORHKAQDLATRTWPCITLFFLLFIPVFCAMHVAQPAVAVLASSRGIAAFVCEY 60
 QY 61 ASFGKATEVAVYLRQADSOVTEVCAATYMGNELTFLDLSICTGSSGNQVNLITIGLR 120
 Db 61 ASFGKATEVAVYLRQADSOVTEVCAATYMGNELTFLDLSICTGSSGNQVNLITIGLR 120
 QY 121 AMDTGILYICKVELMPPPYLYGIGNGAQIYVIDPEPCDPSDFLMTAAVSSGLFFYSFL 180
 Db 121 AMDTGILYICKVELMPPPYLYGIGNGAQIYVIDPEPCDPSDFLMTAAVSSGLFFYSFL 180
 QY 181 LTAVALSKMLKKRSPITTGYYVKNPPTPECECKQFOPIPIPN 223
 Db 181 LTAVALSKMLKKRSPITTGYYVKNPPTPECECKQFOPIPIPN 223

RESULT 3

Q9BDP1 PRELIMINARY; PRT; 223 AA.
 ID Q9BDP1;
 AC Q9BDP1;
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE CD152 protein precursor.
 GN CTLA-4.
 OS Aotus trivirgatus (Night monkey) (Douroucoul).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 NCBI_TaxID=9505;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Boeslik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-Ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344834; AAK37530.1; -;
 DR HSSP; P16410; 1AH1.
 DR InterPro: IPR003599; IG.
 DR SMART; SM00409; IG; 1.
 KW SIGNAL.
 FT SIGNAL.
 SQ SEQUENCE 223 AA; 24813 MW; 3F702052117C1431 CRC64;

Query Match 91.7%; Score 1076; DB 6; Length 223;
 Best Local Similarity 91.5%; Pred. No. 3.9e-101;
 Matches 204; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQDLATRTWPCITLFFLLFIPVFCAMHVAQPAVAVLASSRGIAAFVCEY 60
 Db 1 MACLGFORHKAQDLATRTWPCITLFFLLFIPVFCAMHVAQPAVAVLASSRGIAAFVCEY 60
 QY 61 ASFGKATEVAVYLRQADSOVTEVCAATYMGNELTFLDLSICTGSSGNQVNLITIGLR 120
 Db 61 ASFGKATEVAVYLRQADSOVTEVCAATYMGNELTFLDLSICTGSSGNQVNLITIGLR 120
 QY 121 AMDTGILYICKVELMPPPYLYGIGNGAQIYVIDPEPCDPSDFLMTAAVSSGLFFYSFL 180
 Db 121 AMDTGILYICKVELMPPPYLYGIGNGAQIYVIDPEPCDPSDFLMTAAVSSGLFFYSFL 180
 QY 181 LTAVALSKMLKKRSPITTGYYVKNPPTPECECKQFOPIPIPN 223
 Db 181 LTAVALSKMLKKRSPITTGYYVKNPPTPECECKQFOPIPIPN 223

RESULT 4

Q9XTA1 PRELIMINARY; PRT; 223 AA.
 ID Q9XTA1;
 AC Q9XTA1;
 DT 01-NOV-1999 (T-EMBLrel. 12, Created)
 DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
 DE Cytotoxic T-lymphocyte-associated 4 (Costimulatory molecule B7
 DE receptor CD152).
 GN CTLA4 OR CTLA-4 OR CD152.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NCBI_TaxID=9685;
 [1]
 RP SEQUENCE FROM N.A.
 RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
 RA Mikami T., Takahashi E.;
 RT "Molecular cloning and sequencing of a cDNA encoding the feline
 RT cytotoxic T-lymphocyte-associated 4 (CTLA4) homologue.";
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Choi I.-S., Hash S., Collisson B.W.;
 RT "Sequence analyses of the feline CD28 and CTLA-4.";
 RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:09 ; Search time 47.4949 Seconds
(without alignments)
745.255 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174
Sequence: 1 MACLGFORHKAQLNATRTW.....MPPEPECKQGFQYFIPIN 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	223	22	AA66519 Human CTLA4. Homo
2	1174	100.0	223	23	ABG32819 Human cytotoxic T
3	1174	100.0	223	23	ABG32819 Human cytotoxic T
4	1170	99.7	223	21	AA515129 Human CTLA-4 prote
5	1170	99.7	223	23	AAU74508 Human cytotoxic T-
6	1165	99.2	223	23	AAU74509 Human cytotoxic T-
7	1159	98.7	223	18	AAW25111 Soluble human CTLA
8	1159	98.7	223	22	AAU00687 Human CTLA4 protei
9	1159	98.7	223	23	AB879934 Human CTLA4. Homo

10	1103.5	94.0	234	20	AAV41133 Human CTLA4 protei
11	1034	88.1	223	20	AAV41084 Peline CTLA4 prote
12	1022	87.1	223	20	AAV41083 Canine CTLA4 prote
13	1015	86.5	223	21	AAV32287 Peline CTLA-4. Fe
14	1015	86.5	223	21	AAV32280 Cat CTLA-4 recepto
15	1015	86.5	223	23	AAO17735 Peline CTLA-4. Fe
16	1015	86.5	223	23	AAU78123 Peline cytotoxic T
17	1006	85.7	223	21	AAV15122 Porcine CTLA-4 sol
18	984.5	83.9	211	20	AAW87560 Human CTLA4 recept
19	983	83.7	212	16	AAW60134 CTLA4 receptor fus
20	983	83.7	212	20	AAV43479 Pull length CTLA4
21	983	83.7	212	20	AAW81584 Human CTLA4 recept
22	983	83.7	212	23	ABW78106 Amino acid sequenc
23	983	83.7	212	23	AAU75124 Human CTLA4 recept
24	983	83.7	212	24	ABP56715 Human CTLA4 recept
25	983	83.4	212	14	AAW31040 Human CTLA4 recept
26	979	83.4	212	23	AAU75133 Human CTLA4 recept
27	979	83.4	212	23	AAU75126 Human CTLA4 recept
28	978	83.3	212	23	AAU75132 Human CTLA4 recept
29	977	83.2	212	23	AAU75132 Porcine CTLA4 prot
30	977	83.2	223	22	AAU00686 Human CTLA4 recept
31	976	83.1	212	23	AAU75131 Human CTLA4 recept
32	972	82.8	212	23	AAU75127 Human CTLA4 recept
33	972	82.8	212	23	AAU75129 Human CTLA4 recept
34	971	82.7	212	23	AAU75130 Human CTLA4 recept
35	970	82.6	187	20	AAV41130 Human CTLA4 recept
36	970	82.6	187	20	AAW97615 Human CTLA recepto
37	970	82.6	187	20	AAW97610 Human CTLA recepto
38	969	82.5	212	23	AAU75128 Human CTLA4 recept
39	967	82.4	187	19	AAW69945 Human T cell spect
40	957	81.5	187	19	AAW29728 Soluble CTLA4 muta
41	882	75.1	223	23	ABW79935 Mouse cytotoxic T-
42	878	74.8	223	23	ABG32820 CTLA-4 extracellular
43	837	71.3	168	19	AAW42340 Mouse CTLA4 protei
44	804.5	68.5	234	20	AAV41134 Concatameric immun
45	759	64.7	502	24	ABJ37107

ALIGNMENTS

RESULT 1
ID AAG66519 standard; Protein; 223 AA.
AC AAG66519;
XX 22-OCT-2001 (first entry)
DT Human CTLA4.
XX Human CTLA4.
XX Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
KW immunosuppressive; immunomodulator; anti-allelic; vaccine; antibody;
KW T cell; humanized antibody; autoimmune disorder; graft rejection;
KW allergy.
XX Homo sapiens.
XX OS
XX PN WO200154732-A1.
XX PD 02-AUG-2001.
XX PF 26-JAN-2001; 2001WO-US02653.
XX PR 27-JAN-2000; 2000US-0178473.
XX (GEMT) GENETICS INST INC.
XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
XX O'Hara D, Hinton P, Tsurushita N;
XX WPI; 2001-483195/52.
XX N-PSDB; AAH76437.

XX	Novel antibody-toxic group conjugate comprising an antibody that
PT	recognizes a molecule expressed only on activated T cells, useful for
PT	modulating immune response for treating autoimmune disorder, allergic
PT	response
XX	
XX	
PS	Example 3; Page 114-115; 123pp; English.
CC	The invention relates to an antibody-toxic group conjugate comprising
CC	an antibody that specifically recognises a molecule expressed only on
CC	activated T cells, and a toxic group. The T cell molecule is
CC	preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).
CC	The antibody of the invention is a humanised anti-CTLA4 antibody
CC	comprising a sequence of 128 or 142 amino acids fully defined in the
CC	specification. The antibody-toxic group conjugate is useful for
CC	modulating the immune response in a subject suffering from a disorder
CC	or condition such as autoimmune disorder, immune response to a graft,
CC	allergic response or an immune response to a therapeutic protein.
CC	The antibody is also useful for research purposes, e.g., in staining
CC	and isolating CTLA4-bearing cells. The antibody is also useful for
CC	T-cell typing, for isolating specific IL-2 receptor-bearing cells or
CC	fragments of the receptor, for vaccine preparation, and for determining
CC	the effectiveness of an agent to down-regulate CTLA4 activity. The
CC	present sequence is human CTLA4, which is bound by the antibody
CC	provided in the invention.
SQ	
XX	Sequence 223 AA;
XX	
Query Match	100.0%; Score 1174; DB 22; Length 223;
Best Local Similarity	100.0%; Pred. No. 5.3e-106;
Matches 223:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MACIGFQRHKAQLNATRTWPCITLLIFLLIPVFCANHVAVPAVLASRGIASFVECY 60
DB	1 MACIGFGHHKQGLNATRTWPCITLLIFLLIPVFCANHVAVPAVLASSRGIASFVECY 60
QY	61 ASFGKATVRVTYTFQADSOVTEVCALTYMGMNELTFLDLSICTGTSSGNQNLTIQGR 120
DB	61 ASPGKATVRVTYTFQADSOVTEVCALTYMGMNELTFLDLSICTGTSSGNQNLTIQGR 120
QY	121 AMDPGLYICXELMWPPRYVLGIGNGAQIYYVIDEPCPDSDPLMTLAAVSGLFFYSPL 180
DB	121 AMDPGLYICXELMWPPRYVLGIGNGAQIYYVIDEPCPDSDPLMTLAAVSGLFFYSPL 180
QY	181 LTAVALSIHMLKKRSPLTTGVVYKMPTEBECECKQOPFYFIPIN 223
DB	181 LTAVALSIHMLKKRSPLTTGVVYKMPTEBECECKQOPFYFIPIN 223
RESULT 2	
ID	ABG32819 standard; Protein; 223 AA.
XX	ABG32819;
XX	
D7	23-NOV-2002 (first entry)
DE	
XX	Human cytotoxic T-lymphocyte associated protein, CTLA4.
XX	
KM	Human; cytotoxic T-lymphocyte associated protein; CTLA4;
KM	protein phosphatase 2; PP2A; immune response regulation; gene therapy;
KM	autoimmune thyroiditis; rheumatoid arthritis; myasthenia gravis;
KM	autoimmune chylodietis; systemic lupus erythematosus; Grave's disease;
KM	type I diabetes mellitus; multiple sclerosis; transplant;
KM	graft versus host disease; allergy; inflammatory disorder;
KM	bacterial infection; viral infection; HIV; parasitic infection;
KM	human immunodeficiency virus; hepatitis.
OS	
OS	Homo sapiens.
PH	
FT	Misc-difference 17 Location/Qualifiers
FT	"note="Encoded by GCC"

FT	Misc-difference 91
FT	/note= "Encoded by ACG"
FT	Misc-difference 147
FT	/note= "Encoded by ACC"
PX	
PX	W0200266045-A2.
PN	
PD	29-AUG-2002.
PP	
PR	15-FEB-2002; 2002MO-USO04469.
XX	
XX	16-FEB-2001; 2001US-269757P.
PA	(GEMY) GENETICS INST LLC.
PA	(ROBE-) ROBERTS RES INST JOHN P.
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.
P1	
P1	Collins M, Madrenas J, Carreno B, Kuchroo V;
DR	
DR	WPI; 2002-674892/72.
XX	
XX	N-PSDB; ABSS31629.
PT	
PT	Modulating an immune response, for treating a subject having a
PT	condition that would benefit from down-regulation of an immune
PT	response, e.g. autoimmune disorders, comprises targeting the
PT	interaction between CTLA4 and PP2AA -
XX	
PS	
PS	Disclosure; Page 75-76; 84pp; English.
CC	
CC	The invention relates to modulating an immune response comprising
CC	contacting a cell expressing at least one first molecule having a
CC	CTLA4 (cytotoxic T-lymphocyte associated protein 4) lysine rich
CC	motif, and at least one second molecule having a PP2AA (protein
CC	phosphatase 2A regulatory subunit A) CTLA4-interacting domain with an
CC	agent that modulates the interaction between the first molecule and the
CC	second molecule. Also included are: (1) treating a subject having a
CC	condition that would benefit from down-regulation of an immune response,
CC	comprises administering an agent that inhibits the interaction between a
CC	first molecule and a second molecule described above; (2) identifying a
CC	compound that modulates the interaction of CTLA4 and PP2AA, and
CC	(3) identifying a compound which modulates the interaction of a
CC	molecule comprising at least one CTLA4 lysine rich motif and a PP2AA
CC	molecule comprising a PP2AA CTLA4-interacting domain.
CC	The methods are useful for modulating an immune response and
CC	treating a subject having a condition that would benefit from
CC	down-regulation of an immune response, such as autoimmune thyroiditis,
CC	(e.g. rheumatoid arthritis, myasthenia gravis, autoimmune thyroditis,
CC	systemic lupus erythematosus), type I diabetes mellitus, Grave's
CC	disease, or multiple sclerosis), a transplant (e.g. a bone marrow
CC	transplant, a stem cell transplant, a heart transplant, a lung
CC	transplant, a liver transplant, a kidney transplant, a cornea
CC	transplant, or a skin transplant), graft versus host disease, an
CC	allergy, or an inflammatory disorder. Enhancing an immune
CC	response is useful in treating bacterial, viral (e.g. HIV-1 or -2,
CC	human immunodeficiency virus, hepatitis B or C) or parasitic infections.
CC	The present sequence represents human CTLA4.
CC	
SQ	
SQ	Sequence 223 AA;
Query Match	100.0%; Score 1174; DB 23; Length 223;
Best Local Similarity	100.0%; Pred. No. 5,3e-106;
Matches 223; Conservative	0; Mismatches 0; Indels 0; Gaps 0
D6	
D6	1 MACLGFGHKKQLNLTATRPCTLLFLFLFIPVFCCKAHMVAQPAVLVLASSSRGIASFVCY 60
D6	1 MACLGFGHKKQLNLTATRPCTLLFLFLFIPVFCCKAHMVAQPAVLVLASSSRGIASFVCY 60
OY	
OY	61 ASPEKATEEVRYTVLRQADSOYTEVCATATYMGNSLTFPLDSDICTGTSSGNQVNLTIOGLR 120
Db	
Db	61 ASPEKATEEVRYTVLRQADSOYTEVCATATYMGNSLTFPLDSDICTGTSSGNQVNLTIOGLR 120
OY	
OY	121 AMDPGLYICKEIWMPPPYTYIGNGAIQIVYIDPCDCDSPLMLIIAAVSGLGFYSPL 180
OY	

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:44:30 ; Search time 32.1156 Seconds
(without alignments)
1280.712 Million cell updates/sec

Title: US-09-772-103-2
Perfect score: 1174
Sequence: 1 MACIGFGRHAKQLNLTARTW.....MPTPECEKQFPYFIPIN 223

Scoring table: BLUSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues
Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /published/Applications/AA/*
 - 2: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
 - 5: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
 - 7: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
 - 8: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
 - 9: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
 - 13: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
 - 14: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1174	100.0	223	11	US-09-835-297-2
2	1174	100.0	223	12	US-10-077-106-3
3	1174	100.0	223	15	US-10-211-207-3
4	1159	98.7	223	10	US-09-988-545-21
5	1159	98.7	223	12	US-09-928-267-18
6	1159	98.7	223	12	US-09-928-267-21
7	1159	98.7	223	15	US-10-225-519-8
8	1159	98.7	223	14	US-10-207-655-101
9	1152	98.1	223	14	US-10-107-828-26
10	1152	98.1	223	14	US-10-107-907-26
11	1152	98.1	223	14	US-10-107-907-26
12	1152	98.1	223	15	US-10-107-868-26
13	1015	86.5	223	15	US-10-301-056-26
14	1015	86.5	223	9	US-09-303-510-10
15	983	83.7	212	11	US-09-898-195A-17

16	983	83.7	212	15	US-10-057-288-12	Sequence 12, Appl
17	983	83.7	212	15	US-10-155-514-2	Sequence 2, Appl
18	977	83.2	223	12	US-09-928-267-17	Sequence 17, Appl
19	977	83.2	223	15	US-09-928-267-22	Sequence 22, Appl
20	977	83.2	223	15	US-10-225-519-6	Sequence 6, Appl
21	957	81.5	187	11	US-09-014-761-1	Sequence 1, Appl
22	878	74.8	223	10	US-09-988-545-20	Sequence 20, Appl
23	878	74.8	223	12	US-10-077-106-5	Sequence 5, Appl
24	878	74.8	223	15	US-10-211-207-5	Sequence 7, Appl
25	837	71.3	168	10	US-09-845-899A-7	Sequence 20, Appl
26	759	64.7	502	12	US-10-363-427-20	Sequence 16, Appl
27	753	64.1	377	12	US-10-363-427-16	Sequence 25, Appl
28	735	62.6	502	12	US-10-363-427-24	Sequence 27, Appl
29	682	58.1	271	15	US-10-225-519-25	Sequence 24, Appl
30	678	57.8	377	14	US-10-027-075-24	Sequence 26, Appl
31	667.5	56.9	377	14	US-10-027-075-25	Sequence 28, Appl
32	667	56.8	374	14	US-10-027-075-26	Sequence 316, App
33	663	56.5	382	15	US-10-207-655-316	Sequence 19, Appl
34	663	56.5	382	15	US-10-207-655-316	Sequence 14, Appl
35	661.5	56.3	383	15	US-09-865-321-8	Sequence 4, Appl
36	661.5	56.3	383	11	US-09-898-195A-19	Sequence 16, Appl
37	661.5	56.3	383	15	US-10-057-288-14	Sequence 309, App
38	661.5	56.3	383	15	US-10-155-514-4	Sequence 307, App
39	661.5	56.3	383	15	US-10-155-514-16	Sequence 318, App
40	661	56.3	383	15	US-10-207-655-309	Sequence 13, Appl
41	661	56.3	382	15	US-10-207-655-307	
42	661	56.3	399	15	US-10-207-655-320	
43	661	56.3	403	15	US-10-207-655-318	
44	658	56.0	260	12	US-09-928-267-13	
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ALIGNMENTS

US-09-835-297-2	Sequence 2, Appl
1	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
2	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
3	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
4	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
5	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
6	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
7	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
8	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
9	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
10	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
11	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
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14	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
15	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
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21	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
22	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
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39	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
40	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
41	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
42	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
43	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
44	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY
45	MACIGFGRHAKQLNLTARTWCTLLFLFIPVCKAKHVAQPAVVAASSGIAFVCEY

Db 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
Qy 181 LTAVALSKMLKKRSPLTGGVYVMPPTPECEKQFQPIPIPN 223
Db 181 LTAVALSKMLKKRSPLTGGVYVMPPTPECEKQFQPIPIPN 223

RESULT 2

US-10-077-106-3
; Sequence 3, Application US/10077106
; Publication No. US2003016531A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; FILE REFERENCE: P2A
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/077,106
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269,757
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-106-3

Query Match
Best Local Similarity 100.0%; Score 1174; DB 12; Length 223;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MACLGFORHKAQNLNATRTWPCCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60
Db 1 MACLGFORHKAQNLNATRTWPCCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60
Qy 61 ASFGKATEVRVTVLRQADSVTEVCAATYMGNELTFLLDSICTGTSSGNQVNLTIQGLR 120
Db 61 ASFGKATEVRVTVLRQADSVTEVCAATYMGNELTFLLDSICTGTSSGNQVNLTIQGLR 120
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Db 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
Qy 181 LTAVALSKMLKKRSPLTGGVYVMPPTPECEKQFQPIPIPN 223
Db 181 LTAVALSKMLKKRSPLTGGVYVMPPTPECEKQFQPIPIPN 223

RESULT 3

US-10-211-207-3
; Sequence 3, Application US/10211207
; Publication No. US20030004113A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Madrenas, Joaquin
; APPLICANT: Carreno, Beatriz
; APPLICANT: Kuchroo, Vijay
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
; FILE REFERENCE: GNN-027
; CURRENT APPLICATION NUMBER: US/10/211,207
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: US/10/077,106
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-207-3

Query Match
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Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MACLGFORHKAQNLNATRTWPCCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAAFVCEY 60
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Db 61 ASFGKATEVRVTVLRQADSVTEVCAATYMGNELTFLLDSICTGTSSGNQVNLTIQGLR 120
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RESULT 4

US-09-989-545-21
; Sequence 21, Application US/09989545
; Patent No. US20020164697A1
; GENERAL INFORMATION:
; APPLICANT: Lehar, Sophie
; APPLICANT: Manning, Stephen
; APPLICANT: Coyte, Anthony J.
; APPLICANT: Gutierrez-Ramos, Jose-Carlos
; TITLE OF INVENTION: No. US20020164697A1e1 Th2-Specific Molecules and Uses Thereof
; FILE REFERENCE: 5800-10B
; CURRENT APPLICATION NUMBER: US/09/989,545
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/166,229
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/258,670
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-545-21

Query Match
Best Local Similarity 98.7%; Score 1159; DB 10; Length 223;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 61 ASFGKATEVRVTVLRQADSVTEVCAATYMGNELTFLLDSICTGTSSGNQVNLTIQGLR 120
Db 61 ASFGKATEVRVTVLRQADSVTEVCAATYMGNELTFLLDSICTGTSSGNQVNLTIQGLR 120
Qy 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
Db 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
Qy 181 LTAVALSKMLKKRSPLTGGVYVMPPTPECEKQFQPIPIPN 223
Db 181 LTAVALSKMLKKRSPLTGGVYVMPPTPECEKQFQPIPIPN 223

RESULT 5

US-09-928-267-18
; Sequence 18, Application US/09928267
; Publication No. US20030157705A1
; GENERAL INFORMATION:
; APPLICANT: William, Podor
; TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND
; FILE REFERENCE: 1087-19
; CURRENT APPLICATION NUMBER: US/09/928,267
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 223
; TYPE: PRT
; ORGANISM: human
US-09-928-267-18

Query Match 98.7%; Score 1159; DB 12; Length 223;
Best Local Similarity 98.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNARTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNARTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGTSSGNQVNLTIQGLR 120
DB 61 ASFGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGTSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTGGVYVMPTPECEKQOPYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTGGVYVMPTPECEKQOPYFIPIN 223

RESULT 6
US-09-928-267-21
; Sequence 21, Application US/09928267
; Publication No. US20030157705A1
; GENERAL INFORMATION:
; APPLICANT: William, Podor
; TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND
; FILE REFERENCE: 1087-19
; CURRENT APPLICATION NUMBER: US/09/928,267
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 223
; TYPE: PRT
; ORGANISM: human
US-09-928-267-21

Query Match 98.7%; Score 1159; DB 12; Length 223;
Best Local Similarity 98.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNARTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNARTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGTSSGNQVNLTIQGLR 120
DB 61 ASFGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGTSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180

QY 181 LTAVALSKMLKKRSPLTGGVYVMPTPECEKQOPYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTGGVYVMPTPECEKQOPYFIPIN 223

RESULT 7
US-10-225-519-8
; Sequence 8, Application US/10225519
; Publication No. US20030086940A1
; GENERAL INFORMATION:
; APPLICANT: Costa, Cristina
; APPLICANT: Pizzoloto, Maryellen C.
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CE
; FILE REFERENCE: 33-CIP
; CURRENT APPLICATION NUMBER: US/10/225,519
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 09/928,267
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/29151
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: US 60/161,186
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-519-8

Query Match 98.7%; Score 1159; DB 15; Length 223;
Best Local Similarity 98.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNARTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNARTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGTSSGNQVNLTIQGLR 120
DB 61 ASFGKATEVRVTVLRQADSQVTEVCATYTMGNELTFDDSICTGTSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPYYLIGNGAQIYVIDPEPCPSDFLMTLAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTGGVYVMPTPECEKQOPYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTGGVYVMPTPECEKQOPYFIPIN 223

RESULT 8
US-10-207-655-101
; Sequence 101, Application US/10207655
; Publication No. US20030118592A1

; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 39069, 401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-101

Query Match 98.7%; Score 1159; DB 15; Length 223;
Best Local Similarity 98.7%; Pred. No. 1,2e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
DB 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
QY 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
DB 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBCEKQOPFYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBCEKQOPFYFIPIN 223

RESULT 9

US-10-107-828-26
; Sequence 26, Application US/10107828
; Publication No. US20020115831A1
; GENERAL INFORMATION:
; APPLICANT: Tamatani, Takuya
; TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL
; FILE REFERENCE: 06501-039002
; CURRENT APPLICATION NUMBER: US/10/107,828
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US/09/561,308B
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/JP98/00837
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: JAPAN 09-62290
; PRIOR FILING DATE: 1997-02-27
; PRIOR APPLICATION NUMBER: JAPAN 10-62217
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-828-26

Query Match 98.1%; Score 1152; DB 14; Length 223;
Best Local Similarity 98.2%; Pred. No. 6,1e-111;
Matches 219; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
DB 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
QY 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
DB 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBCEKQOPFYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBCEKQOPFYFIPIN 223

RESULT 10
US-10-107-907-26
; Sequence 26, Application US/10107907

Publication No. US20020151685A1
; GENERAL INFORMATION:
; APPLICANT: Tamatani, Takuya
; TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL
; FILE REFERENCE: 06501-039002
; CURRENT APPLICATION NUMBER: US/10/107,907
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/561,308
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/JP98/00837
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: JAPAN 09-62290
; PRIOR FILING DATE: 1997-02-27
; PRIOR APPLICATION NUMBER: JAPAN 10-62217
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-107-907-26

Query Match 98.1%; Score 1152; DB 14; Length 223;
Best Local Similarity 98.2%; Pred. No. 6,1e-111;
Matches 219; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
DB 1 MACLGFORHKAQNLNATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY 60
QY 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
DB 61 ASFGKATEYRVTVLRQADSOVTEVCATYTMGNELTFLLDSICTGTSSGNQVNLTIQGR 120
QY 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
DB 121 AMDTGXYICKVELMPPPYLIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBCEKQOPFYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBCEKQOPFYFIPIN 223

RESULT 11

US-10-107-868-26
; Sequence 26, Application US/10107868
; Publication No. US20020156242A1
; GENERAL INFORMATION:
; APPLICANT: Tamatani, Takuya
; TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL
; FILE REFERENCE: 06501-039002
; CURRENT APPLICATION NUMBER: US/10/107,868
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/561,308
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 09/383,551
; PRIOR FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: PCT/JP98/00837
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: JAPAN 09-62290
; PRIOR FILING DATE: 1997-02-27
; PRIOR APPLICATION NUMBER: JAPAN 10-62217
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 223
; TYPE: PRT

ORGANISM: Homo sapiens
US-10-107-868-26

Query Match 98.1%; Score 1152; DB 14; Length 223;
Best Local Similarity 98.2%; Pred. No. 6.1e-111;
Matches 219; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCCTLLFLLFPIVPCCKAMHVAQPAVVLASSRGIAAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCCTLLFLLFPIVPCCKAMHVAQPAVVLASSRGIAAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLTIQGLR 120
DB 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPPYTLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYTLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
QY 121 AMDTGLYICKVELMPPPYTLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYTLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKOFOPYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKOFOPYFIPIN 223

RESULT 12

US-10-301-056-26
Sequence 26, Application US/10301056
Publication No. US20030083472A1

GENERAL INFORMATION:
APPLICANT: Tamaki, Takuya
TITLE OF INVENTION: CELL SURFACE MOLECULE MEDIATING CELL
FILE REFERENCE: 06501-039001
CURRENT APPLICATION NUMBER: US/10/301,056
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/383,551
PRIOR FILING DATE: 1999-08-26
PRIOR APPLICATION NUMBER: PCT/JP98/00837
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: JAPAN 09-62290
PRIOR FILING DATE: 1997-02-27
PRIOR APPLICATION NUMBER: JAPAN 10-62217
PRIOR FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 223
TYPE: PRT
ORGANISM: Homo sapiens
US-10-301-056-26

Query Match 98.1%; Score 1152; DB 15; Length 223;
Best Local Similarity 98.2%; Pred. No. 6.1e-111;
Matches 219; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCCTLLFLLFPIVPCCKAMHVAQPAVVLASSRGIAAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCCTLLFLLFPIVPCCKAMHVAQPAVVLASSRGIAAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLTIQGLR 120
DB 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPPYTLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYTLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKOFOPYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKOFOPYFIPIN 223

RESULT 13

US-09-303-510-10
Sequence 10, Application US/09303510A
Patent No. US20020028208A1

GENERAL INFORMATION:
APPLICANT: Collision, Ellen W.
TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptides
FILE REFERENCE: 54954
CURRENT APPLICATION NUMBER: US/09/303,510A
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,869
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 223
TYPE: PRT
ORGANISM: feline
US-09-303-510-10

Query Match 86.5%; Score 1015; DB 9; Length 223;
Best Local Similarity 85.7%; Pred. No. 9e-97;
Matches 191; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCCTLLFLLFPIVPCCKAMHVAQPAVVLASSRGIAAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCCTLLFLLFPIVPCCKAMHVAQPAVVLASSRGIAAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLTIQGLR 120
DB 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELFLDSDICTGTSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPPYTLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPYTLGIGNGAQIYVIDPEPCDSDFLMILAASSGLFFYSFL 180
QY 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKOFOPYFIPIN 223
DB 181 LTAVALSKMLKKRSPLTTGVVYKMPTEBECEKOFOPYFIPIN 223

RESULT 14

US-09-303-040-10
Sequence 10, Application US/09303040
Patent No. US20020051792A1

GENERAL INFORMATION:
APPLICANT: Winslow, Barbara J.
TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
TITLE OF INVENTION: feline CD80, feline CD86, feline CD28, feline CTLA-4 or
FILE REFERENCE: 54957-B
CURRENT APPLICATION NUMBER: US/09/303,040
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,870
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 223
TYPE: PRT
ORGANISM: feline CTLA-4
US-09-303-040-10

Query Match 86.5%; Score 1015; DB 9; Length 223;
Best Local Similarity 85.7%; Pred. No. 9e-97;
Matches 191; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQNLATRTWPCCTLLFLLFPIVPCCKAMHVAQPAVVLASSRGIAAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCCTLLFLLFPIVPCCKAMHVAQPAVVLASSRGIAAFVCEY 60


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Db      1 MACGRRRGAQDLDASRTWPCIALFSLFIPVFSKGMHVAHPAVVLASSRGVASFVCEY 60
Qy      61 ASPGKATEVRVTVLRQADSVTEVCATYMMGNELTFLDISICTGSSGNQVNLITQGLR 120
      61 GSSGNNAKFRVTVLRQTSQMTVCATYVENELAFINDSTCTGSSGNQVNLITQGLR 120
Qy      121 AMDTGLYICKVELMYPPIYLGINGAQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFL 180
      121 AMDTGLYICKVELMYPPIYAGMGNGTQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFL 180
Db      181 LTAVSLSKMLKKRSLTTGVYVMPTPECEKQFPYFIPIN 223
      181 ITAVSLSKMLKKRSLTTGVYVMPTPECEKQFPYFIPIN 223
```

RESULT 15

```
US-09-898-195A-17
; Sequence 17, Application US/09898195A
; Publication No. US20030083246A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Robert
; APPLICANT: Carr, Suzanne
; APPLICANT: Hagetty, David
; APPLICANT: Beach, Robert J
; APPLICANT: Becker, Jean-Claude
; TITLE OF INVENTION: METHODS FOR TREATING RHEUMATIC DISEASES USING A SOLUBLE
; FILE REFERENCE: D0030NP/30436.55USU1
; CURRENT APPLICATION NUMBER: US/09/898,195A
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/215,913
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-195A-17
```

Query Match 83.7%; Score 983; DB 11; Length 212;

Best Local Similarity 91.9%; Pred. No. 1.7e-93;

Matches 192; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

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Qy      15 LATRTWPCITLFLFIPVCKAMHVAOPAVVLASSRGIASFVCEYASPGKATEVRVTVL 74
      4 LRTQRTLLSLVIALLPSSAMAMHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVL 63
Qy      75 ROADSVTEVCATYMMGNELTFLDISICTGSSGNQVNLITQGLRAMDGLYICKVELM 134
      64 ROADSVTEVCATYMMGNELTFLDISICTGSSGNQVNLITQGLRAMDGLYICKVELM 123
Qy      135 YPPPYLIGINGAQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFLITAVSLSKMLKKRS 194
      124 YPPPYLIGINGAQIYVIDPEPCPDSDFLLMILAAVSSGLFFYSFLITAVSLSKMLKKRS 183
Qy      195 PLTTGVYVMPTPECEKQFPYFIPIN 223
      184 PLTTGVYVMPTPECEKQFPYFIPIN 212
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Search completed: December 2, 2003, 06:56:44
Job time : 32.1156 secs

Query Match 98.6%; Score 1158; DB 3; Length 223;
Best Local Similarity 98.7%; Pred. No. 5.5e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCAKMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCAKMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSVTEVCAATYMMGNELTFLDLS-ICTGTSSGNQVNLTIQGLR 120
DB 61 ASFGKATEVRVTVLRQADSVTEVCAATYMMGNELTFLDLS-ICTGTSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCPSDFLLMTLAAVSSGLPFYSFL 180
DB 121 AMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPEPCPSDFLLMTLAAVSSGLPFYSFL 180
QY 181 LTAVALSKMLKKRSPPLTTGVYVYMPPEBCECKQFPYFPIPIN 223
DB 181 LTAVALSKMLKKRSPPLTTGVYVYMPPEBCECKQFPYFPIPIN 223

RESULT 2

US-08-505-058-1
; Sequence 1, Application US/08505058
; Patent No. 5773253
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Peach, Robert
; TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,058
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/228,208
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-505-058-1

Query Match 94.0%; Score 1103.5; DB 1; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCAKMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCAKMHVAQPAVVLASSRGIAFVCEY 60

DB 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCAKMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSVTEVCAATYMMGNELTFLDLS-ICTGTSSGNQVNLTIQGLR 118
DB 61 ASFGKATEVRVTVLRQADSVTEVCAATYMMGNELTFLDLS-ICTGTSSGNQVNLTIQGLR 120
QY 119 LRAMDGLYICKVELMPPPYLLGIGNGAQIYVIDPEPC-PSDFLLMTLAAVSS 172
DB 121 LRAMDGLYICKVELMPPPYLLGIGNGAQIYVIDPEPC-PSDFLLMTLAAVSS 180
QY 173 GLFFYSFLITLTAVALSKMLKKRSPPLTTGVYVYMPPEBCECKQFPYFPIPIN 223
DB 181 GLFFYSFLITLTAVALSKMLKKRSPPLTTGVYVYMPPEBCECKQFPYFPIPIN 224

RESULT 3

US-08-459-818-21
; Sequence 21, Application US/08459818
; Patent No. 5851795
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Dame, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeg 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,818
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-818-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCAKMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACIGFQRHKAQNLNATRTWPCITLLFLLPIVPCAKMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSVTEVCAATYMMGNELTFLDLS-ICTGTSSGNQVNLTIQGLR 118
DB 61 ASFGKATEVRVTVLRQADSVTEVCAATYMMGNELTFLDLS-ICTGTSSGNQVNLTIQGLR 120
QY 119 LRAMDGLYICKVELMPPPYLLGIGNGAQIYVIDPEPC-PSDFLLMTLAAVSS 172
DB 121 LRAMDGLYICKVELMPPPYLLGIGNGAQIYVIDPEPC-PSDFLLMTLAAVSS 180

Tue Dec 2 07:01:18 2003

us-09-772-103-2.rat

Page 3

QY 173 GLFFYSFLTT-AVSLSKMLKKRSPLTGGVYVMPTEPECE--KOFOPYFIPIN 223
Db 181 GLFFYSFLTTAAVSLSKMLKKRSPLTGGVYVMPTEPECEKXKOPFYFIPIN 234

RESULT 4
US-08-889-666-21
; Sequence 21, Application US/08889666
; Patent No. 5885379
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Dangle, Milton K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,666
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-889-666-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQNLNATRTWPCCTLLFLLFIPVPCAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQNLNATRTWPCCTLLFLLFIPVPCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSVTEVCATYTMGNELTFLDSDXICTGTSSGNQVNLITIG 118
Db 61 ASFGKATEVRVTVLRQADSVTEVCATYTMGNELTFLDSDXICTGTSSGNQVNLITIG 120
QY 119 LRAMDGTLYICKVELMPPPYTL-GINGAQIYVIDPEPC-----PQSDFLMLTAAVSS 172
Db 121 LRAMDGTLYICKVELMPPPYTLGIGNGTOIYVIDPEPCXXXXXPDSDFLMLTAAVSS 180
QY 173 GLFFYSFLTT-AVSLSKMLKKRSPLTGGVYVMPTEPECE--KOFOPYFIPIN 223
Db 181 GLFFYSFLTTAAVSLSKMLKKRSPLTGGVYVMPTEPECEKXKOPFYFIPIN 234

RESULT 5
US-08-465-078-21
; Sequence 21, Application US/08465078
; Patent No. 5885796
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Dangle, Milton K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,078
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-078-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQNLNATRTWPCCTLLFLLFIPVPCAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQNLNATRTWPCCTLLFLLFIPVPCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSVTEVCATYTMGNELTFLDSDXICTGTSSGNQVNLITIG 118
Db 61 ASFGKATEVRVTVLRQADSVTEVCATYTMGNELTFLDSDXICTGTSSGNQVNLITIG 120
QY 119 LRAMDGTLYICKVELMPPPYTL-GINGAQIYVIDPEPC-----PQSDFLMLTAAVSS 172
Db 121 LRAMDGTLYICKVELMPPPYTLGIGNGTOIYVIDPEPCXXXXXPDSDFLMLTAAVSS 180
QY 173 GLFFYSFLTT-AVSLSKMLKKRSPLTGGVYVMPTEPECE--KOFOPYFIPIN 223
Db 181 GLFFYSFLTTAAVSLSKMLKKRSPLTGGVYVMPTEPECEKXKOPFYFIPIN 234
RESULT 6
US-08-725-776-21
; Sequence 21, Application US/08725776

```
Patent No. 5968510
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-725-776-21

Query Match          94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQNLATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELTFPLDSS--ICTGTSSGNOVNLTIQ 118
DB 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELTFPLDSSXXICTGTSSGNOVNLTIQ 120
QY 119 LRAMDGLYICKVEMLPYPYTL-GINGAQIYVIDPPEC-----PDSDFLMTILAAVSS 172
DB 121 LRAMDGLYICKVEMLPYPYTLXGINGQIYVIDPPECXXXXXPSDFLMTILAAVSS 180
QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTGTVVKKMPTEBECE--KOPQYFPIPIN 223
DB 181 GLFFYSFLLTAVSLSKMLKKRSPLTGTVVKKMPTEBECEXXKQOFYFPIPIN 234

RESULT 7
US-08-488-062-21
Sequence 21, Application US/08488062
Patent No. 5977318
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
```

```
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 1150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,062
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-062-21

Query Match          94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 2.3e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQNLATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACLGFORHKAQNLATRTWPCITLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELTFPLDSS--ICTGTSSGNOVNLTIQ 118
DB 61 ASFGKATEVRVTVLRQADSOVTEVCATYTMGNELTFPLDSSXXICTGTSSGNOVNLTIQ 120
QY 119 LRAMDGLYICKVEMLPYPYTL-GINGAQIYVIDPPEC-----PDSDFLMTILAAVSS 172
DB 121 LRAMDGLYICKVEMLPYPYTLXGINGQIYVIDPPECXXXXXPSDFLMTILAAVSS 180
QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTGTVVKKMPTEBECE--KOPQYFPIPIN 223
DB 181 GLFFYSFLLTAVSLSKMLKKRSPLTGTVVKKMPTEBECEXXKQOFYFPIPIN 234

RESULT 8
US-09-303-040-10
Sequence 10, Application US/09303040
Patent No. 655671
GENERAL INFORMATION:
APPLICANT: Winslow, Barbara J.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
FILE REFERENCE: 54957-B
CURRENT APPLICATION NUMBER: US/09/303,040
CURRENT FILING DATE: 1999-04-30
```

EARLIER APPLICATION NUMBER: 60/083,870
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 223
TYPE: PRT
ORGANISM: feline CTLA-4
US-09-103-040-10

Query Match 86.5%; Score 1015; DB 4; Length 223;
Best Local Similarity 85.7%; Pred. No. 2.6e-96;
Matches 191; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 1 MACLGROHRAQANTLRTMPCULLFLLFIPPCAMHVAQAVVLASSRGIASTVCEY 60
DB 1 MACFGRRRHQAQDLASRTMPCALFSLFIPFSGMHAHVAVVLASSRGVASFVCEY 60
QY 61 ASPKATEVRVTVLRQADSOVTEVCAATYMGNELTFLDLSICTGSSGNOVLTIOGR 120
DB 61 GSGGNNAKRRVTVLRQDGSMTVCATTYVENELAFINDSTCTGSSGKNVLTIOGR 120
QY 121 AMDTGILYICKVELMPPPYLLGIGNGAQIYVIDPBCPDSPFLMILAAVSSGLFFYSFL 180
DB 121 AMDTGILYICKVELMPPPYLLGIGNGAQIYVIDPBCPDSPFLMILAAVSSGLFFYSFL 180
QY 181 LRAVSLSKMLKRSPLTGYVYVMPTPECEKOPPIPIPN 223
DB 181 ITAVSLSKMLKRSPLTGYVYVMPTPECEKOPPIPIPN 223

RESULT 9

US-08-067-684-14
Sequence 14, Application US/08067684
Patent No. 5434131
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Nalin K.
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, Suite 900
CITY: Pasadena
STATE: California
COUNTRY: U.S.A.
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/067,684
FILING DATE: 26-MAY-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 7848-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310/312-9900
TELEFAX: 310/479-8340
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-067-684-14

Query Match 82.6%; Score 970; DB 1; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIASTVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMGNELT 96
DB 1 AMHVAQPAVVLASSRGIASTVCEYASPGKATEVRVTVLRQADSOVTEVCAATYMGNELT 96
QY 97 FLDDSICTSSGNOVLTIOGLRAMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPBP 156
DB 61 FLDDSICTSSGNOVLTIOGLRAMDTGLYICKVELMPPPYLLGIGNGAQIYVIDPBP 120
QY 157 CPDSDFLMILAAVSSGLFFYSFLITAVSLSKMLKRSPLTGYVYVMPTPECEKOPQ 216
DB 121 CPDSDFLMILAAVSSGLFFYSFLITAVSLSKMLKRSPLTGYVYVMPTPECEKOPQ 180
QY 217 PYPIPIPN 223
DB 181 PYPIPIPN 187

RESULT 10

US-08-008-898-14
Sequence 14, Application US/08008898
Patent No. 5770197
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Dame, Nalin K.
TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 201 South Lake Avenue, Suite 800
CITY: Pasadena
STATE: California
COUNTRY: United States
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/008,898
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/723,617
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandel, Saralynn
REGISTRATION NUMBER: 31,853
REFERENCE/DOCKET NUMBER: 7848
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
TELEFAX: (818) 795-6321
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-008-898-14
Query Match 82.6%; Score 970; DB 1; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60
Qy 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPEPYLLGIGNGAQIYVIDPPE 156
Db 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPEPYLLGIGNGAQIYVIDPPE 120
Qy 157 CPDSDFLMLTAAVSSGLFFYSFLLTAVSLSKMLKKRSPLLTGVYVVMPPTEPECEKQFO 216
Db 121 CPDSDFLMLTAAVSSGLFFYSFLLTAVSLSKMLKKRSPLLTGVYVVMPPTEPECEKQFO 180
Qy 217 PYFIPIN 223
Db 181 PYFIPIN 187

RESULT 11
US-08-459-818-14
Sequence 14, Application US/08459818
Patent No. 5851795
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Milton K.
APPLICANT: Brady, William
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Fastseq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-818-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 96
Db 1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60
Qy 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPEPYLLGIGNGAQIYVIDPPE 156
Db 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPEPYLLGIGNGAQIYVIDPPE 120
Qy 157 CPDSDFLMLTAAVSSGLFFYSFLLTAVSLSKMLKKRSPLLTGVYVVMPPTEPECEKQFO 216
Db 121 CPDSDFLMLTAAVSSGLFFYSFLLTAVSLSKMLKKRSPLLTGVYVVMPPTEPECEKQFO 180

Qy 217 PYFIPIN 223
Db 181 PYFIPIN 187

RESULT 12
US-08-889-666-14
Sequence 14, Application US/08889666
Patent No. 588579
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Milton K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,666
FILING DATE: 08-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-889-666-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 96
Db 1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMMGNELT 60
Qy 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPEPYLLGIGNGAQIYVIDPPE 156
Db 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVBLMYPPEPYLLGIGNGAQIYVIDPPE 120
Qy 157 CPDSDFLMLTAAVSSGLFFYSFLLTAVSLSKMLKKRSPLLTGVYVVMPPTEPECEKQFO 216
Db 121 CPDSDFLMLTAAVSSGLFFYSFLLTAVSLSKMLKKRSPLLTGVYVVMPPTEPECEKQFO 180
Qy 217 PYFIPIN 223
Db 181 PYFIPIN 187

RESULT 13
US-08-465-078-14
Sequence 14, Application US/08465078
Patent No. 5685796
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kienner, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,078
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-078-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMGNELT 96
DB 1 AMHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMGNELT 60
QY 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPRYLIGINGAQIYVIDPFP 156
DB 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPRYLIGINGAQIYVIDPFP 120
QY 157 CPDSDFLMILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTGGVYKMPTEPECEKQFO 216
DB 121 CPDSDFLMILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTGGVYKMPTEPECEKQFO 180
QY 217 PYFIPIN 223
DB 181 PYFIPIN 187

RESULT 14
US-08-725-776-14
Sequence 14, Application US/08725776
Patent No. 5968510
GENERAL INFORMATION:

APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kienner, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-725-776-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 8.3e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMGNELT 96
DB 1 AMHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCATYMGNELT 60
QY 97 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPRYLIGINGAQIYVIDPFP 156
DB 61 FLDDSICTGTSSGNQVNLITQGLRAMDTGLYICKVELMPPRYLIGINGAQIYVIDPFP 120
QY 157 CPDSDFLMILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTGGVYKMPTEPECEKQFO 216
DB 121 CPDSDFLMILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTGGVYKMPTEPECEKQFO 180
QY 217 PYFIPIN 223
DB 181 PYFIPIN 187

RESULT 15
US-08-488-062-14
Sequence 14, Application US/08488062
Patent No. 5977318
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kienner, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:39:15 ; Search time 9.08722 Seconds
(without alignments)
1354.605 Million cell updates/sec

Title: US-09-772-103-8

Perfect score: 655

Sequence: 1 MDFQVQIFSFLLISAVILS.....COQMSYPLTFGGTKVLEIK 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	502	76.6	130	2	A32513
2	499	76.2	130	1	JL0079
3	498	76.0	235	2	S25058
4	491	75.0	140	2	PL0013
5	478	73.0	130	2	S04573
6	466	71.1	130	2	B32456
7	463.5	70.8	107	2	S36264
8	463.5	70.8	107	2	S36264
9	463.5	70.8	108	2	B49047
10	455.5	69.5	129	2	S40349
11	454.5	69.4	107	2	S52793
12	454.5	69.4	129	2	S40317
13	454.5	69.4	129	2	S52789
14	452.5	69.1	123	2	S40331
15	452.5	69.1	125	2	S40334
16	451.5	68.9	108	2	S19674
17	451.5	68.9	132	2	S40334
18	447.5	68.3	125	2	S40316
19	446	68.1	129	1	KWMS78
20	445.5	68.0	127	1	S40367
21	444.5	67.9	108	1	KIHUR7
22	444.5	67.9	108	1	S36277
23	441.5	67.4	108	1	KIHUN8
24	441.5	67.4	117	2	S46371
25	441.5	67.4	125	2	S40350
26	441.5	67.3	132	2	S05268
27	439.5	67.1	129	2	S40369
28	437.5	66.8	108	2	S36279
29	436.5	66.6	108	1	KIHUNE

30	436	66.6	106	2	PC2397	anti-tetanus toxin
31	435.5	66.5	107	2	I59017	anti-HIV1 envelope
32	435.5	66.5	108	1	KIHUN9	Ig kappa chain V-I
33	435.5	66.5	125	2	S40353	Ig kappa chain V-J
34	434.5	66.3	110	2	S44118	Ig kappa chain V-J
35	434.5	66.3	117	2	S46376	Ig kappa chain V-J
36	434.5	66.3	123	2	S40313	Ig kappa chain V-J
37	432.5	66.0	108	1	KIHUN10	Ig kappa chain V-I
38	431	65.8	109	1	KIHUN11	Ig kappa chain V-I
39	430.5	65.7	109	2	S31998	Ig kappa chain V-I
40	430.5	65.7	129	1	KIHUN12	Ig kappa chain - h
41	430	65.6	124	2	S40336	Ig kappa chain pre
42	429.5	65.6	108	2	S44122	Ig kappa chain V-J
43	429.5	65.6	131	2	S40352	Ig kappa chain V-I
44	429.5	65.6	139	2	S40365	Ig kappa chain V-J
45	429.5	65.6	141	2	A49134	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

A32513

Ig kappa chain precursor V region (MRU22) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C/Accession: A32513

R/Kofler, R.; Strohal, R.; Balderae, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;

J. Clin. Invest. 82, 852-860, 1988

A/Title: Immunoglobulin kappa light chain variable region gene complex organization and

A/Reference number: A94669; MUID:88331394; PMID:3138286

A/Accession: A32513

A/Molecule type: DNA

A/Residues: 1-130 <KOF>

A/Cross-references: GB:M20834; NID:g196943; PID:AAA3846.1; PID:g196944

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 502; DB 2; Length 130;

Best Local Similarity 74.6%; Pred. No. 2.7e-33;

Matches 97; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

Qy	1	MDFQVQIFSFLLISAVILSRGDIQMTQSPFSLASVGDRTVITCSATSI--TYMSYQ	58
Db	1	MDFQVQIFSFLLISAVILSRGQIVLTQSPALMSAEGERTVITCSASSVSTLYIQ	60
Qy	59	OKPKAPKLLIYDTSNLASGVPSRFSGSGCTDYTLTISLQPPDFATYYCOQMSYPLT	118
Db	61	OKPSSPKLMTYTSNLASGVPARFSGSGCTSYSLTISMEADDAITYCQVSGVPFT	120
Qy	119	FGGCTKVEIK 128	
Db	121	FGTGTKEIK 130	

RESULT 2
JL0079
Ig kappa chain precursor V region (anti-phenylloxazalone 6f6) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C/Accession: JL0079; A49044; B49044
R/Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A/Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re;
A/Reference number: JL0076; MUID:89096973; PMID:3211160
A/Accession: JL0079
A/Molecule type: mRNA
A/Residues: 1-130 <KAA>
A/Cross-references: GB:M27792; NID:g197159
A/Experimental source: mRNA clones for anti-phenylloxazalone antibody 6f6
A/Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10
A/Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation

R.Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
 Eur. J. Immunol. 22, 1627-1634, 1992
 A>Title: Non-random features of the repertoire expressed by the members of one V kappa g
 A:Reference number: A49044; MUID:92289826; PMID:1601044
 A:Accession: A49044
 A:Molecule type: DNA
 A:Residues: 1-25 <MTL>
 A:Cross-references: GB:S37663; NID:g250214; PIDN:AA822332.1; PID:g250217
 A>Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBI:106809)
 A:Accession: B49044
 A:Molecule type: DNA
 A:Residues: 114-116 <ML2>
 A:Cross-references: GB:S37664; NID:g250215; PIDN:AA822332.1; PID:g250218
 A:Experimental source: BALB/c germ-line
 A>Note: sequences extracted from NCBI backbone: partial nucleotide sequences of 13 addit
 A>Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBI:106822)
 C:Genetics:
 A:Gene: V(Kappa)Ox1
 A:Introns: 17/1
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (Kap
 hain disulfide bonds. In some cases, such as Iga and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
 F:38-111/Domain: immunoglobulin homology <IMM>
 F:45-109/Domain: #status predicted

Query Match 76.2%; Score 499; DB 1; Length 130;
 Best Local Similarity 74.2%; Pred. No. 4.7e-33;
 Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MDPVOVIFSLIISAVILSRGDIOMTOSPSLSASVGDRTVITCSATSYTMSWYQOK 60
 Db 1 MDPVOVIFSLIISAVILSRGDIOMTOSPSLSASVGDRTVITCSATSYTMSWYQOK 60

Qy 61 PGKAPKLLIYDTSNLSAGVPSRFGSGSGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
 Db 61 SGTSPKRWIYDTSKLSAGVPSRFGSGSGSYSLTISMEADATYTCQOMSSYPLTFG 120

Qy 121 GGTVEIK 128
 Db 121 AGTKLEK 128

RESULT 3
 S25058
 Ig kappa chain - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
 C:Accession: S25058
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
 Submitted to the EMBL Data Library, July 1992
 A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neoprotein specific
 A:Reference number: S25057
 A:Accession: S25058
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-235 <PIS>
 A:Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 498; DB 2; Length 235;
 Best Local Similarity 74.2%; Pred. No. 9.9e-33;
 Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MDPVOVIFSLIISAVILSRGDIOMTOSPSLSASVGDRTVITCSATSYTMSWYQOK 60
 Db 1 MDPVOVIFSLIISAVILSRGDIOMTOSPSLSASVGDRTVITCSATSYTMSWYQOK 60

Qy 61 PGKAPKLLIYDTSNLSAGVPSRFGSGSGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
 Db 61 SGTSPKRWIYDTSKLSAGVPSRFGSGSGSYSLTISMEADATYTCQOMSSYPLTFG 120

Db 61 SGTSPKRWIYDTSKLSAGVPSRFGSGSGSYSLTISMEADATYTCQOMSSYPLTFG 120
 Qy 121 GGTVEIK 128
 Db 121 AGTKLEK 128

RESULT 4
 PL0013
 Ig kappa chain precursor V region (4C11) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
 C:Accession: PL0013
 R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kleber-Emmons, T.; Kohler, H.
 Mol. Immunol. 25, 33-40, 1988
 A>Title: Structural basis of stimulatory anti-idiotypic antibodies.
 A:Reference number: PL0011; MUID:86142853; PMID:3125424
 A:Accession: PL0013
 A:Molecule type: mRNA
 A:Residues: 1-140 <CHB>
 A:Experimental source: cell line 4C11
 C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
 F:38-111/Domain: immunoglobulin homology <IMM>
 F:46-55/Region: complementarity-determining 1
 F:71-77/Region: complementarity-determining 2
 F:110-118/Region: complementarity-determining 3
 F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 75.0%; Score 491; DB 2; Length 140;
 Best Local Similarity 74.2%; Pred. No. 2.2e-33;
 Matches 95; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MDPVOVIFSLIISAVILSRGDIOMTOSPSLSASVGDRTVITCSATSYTMSWYQOK 60
 Db 1 MDPVOVIFSLIISAVILSRGDIOMTOSPSLSASVGDRTVITCSATSYTMSWYQOK 60

Qy 61 PGKAPKLLIYDTSNLSAGVPSRFGSGSGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
 Db 61 PDIKPKMIYDTSNLSAGVPSRFGSGSGSYSLTISMEADATYTCQOMSSYPLTFG 120

Qy 121 GGTVEIK 128
 Db 121 GGTLEMK 128

RESULT 5
 S04573
 Ig kappa chain precursor V region (MRL-histone 7L) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
 C:Accession: S04573
 R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balders, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
 Eur. J. Immunol. 17, 91-95, 1987
 A>Title: Molecular analysis of the murine lupus-associated anti-self response: involvem
 A:Reference number: S04573; MUID:87133856; PMID:3102255
 A:Accession: S04573
 A:Molecule type: mRNA
 A:Residues: 1-130 <KOF>
 A:Cross-references: EMBL:X14620; NID:g25031; PIDN:CAA32773.1; PID:g25032
 A>Note: the authors translated the codon AGC for residue 47 as Aen
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
 F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 478; DB 2; Length 130;
 Best Local Similarity 70.8%; Pred. No. 2.2e-31;
 Matches 92; Conservative 22; Mismatches 14; Indels 2; Gaps 1;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:49 ; Search time 5.9716 Seconds

(without alignment)
1008.007 Million cell updates/sec

Title: US-09-772-103-8

Perfect score: 655

Sequence: 1 MDPQVQIFSFLLISAVLIS.....COQMSYPLTFCGTRKVEIK 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	446	68.1	129	KV4A_MOUSE	P01680 mus musculu
2	444.5	67.9	108	KV1P_HUMAN	P01608 homo sapien
3	441.5	67.4	108	KV1O_HUMAN	P04330 homo sapien
4	436.5	66.6	108	KV1V_HUMAN	P01607 homo sapien
5	435.5	66.5	108	KV1B_HUMAN	P01594 homo sapien
6	434.5	66.3	108	KV1Y_HUMAN	P80362 homo sapien
7	432.5	66.0	108	KV1H_HUMAN	P01600 homo sapien
8	431	65.8	109	KV1T_HUMAN	P01612 homo sapien
9	430.5	65.7	129	KV1X_HUMAN	P04332 homo sapien
10	427.5	65.3	108	KV1S_HUMAN	P01611 homo sapien
11	427.5	65.3	129	KV1W_HUMAN	P04331 homo sapien
12	422.5	64.5	108	KV1F_HUMAN	P01598 homo sapien
13	422.5	64.5	108	KV1G_HUMAN	P01605 homo sapien
14	421.5	64.4	108	KV1I_HUMAN	P01599 homo sapien
15	421.5	64.4	108	KV1R_HUMAN	P01610 homo sapien
16	420.5	64.2	108	KV1L_HUMAN	P01593 homo sapien
17	418.5	63.9	108	KV1A_HUMAN	P01604 homo sapien
18	416	63.5	107	KV1D_HUMAN	P01596 homo sapien
19	413.5	63.1	108	KV1K_HUMAN	P01603 homo sapien
20	412.5	63.0	108	KV1E_HUMAN	P01597 homo sapien
21	412.5	63.0	108	KV1N_HUMAN	P01606 homo sapien
22	412	62.9	108	KV1Q_HUMAN	P04945 mus musculu
23	409.5	62.5	108	KV1C_HUMAN	P01609 homo sapien
24	408.5	62.4	108	KV1J_HUMAN	P01595 mus musculu
25	408.5	62.4	108	KV1J_HUMAN	P01643 mus musculu
26	408.5	62.4	117	KV1J_HUMAN	P01602 homo sapien
27	401.5	61.3	117	KV1I_HUMAN	P01601 homo sapien
28	399	60.9	107	KV1F_HUMAN	P04940 mus musculu
29	398.5	60.8	112	KV1U_HUMAN	P01613 mus musculu
30	394	60.2	107	KV1I_HUMAN	P04943 mus musculu
31	393	60.0	107	KV1G_HUMAN	P04941 mus musculu
32	393	60.0	107	KV1G_HUMAN	P04942 mus musculu
33	392	59.8	107	KV6J_MOUSE	P04944 mus musculu

34	389	59.4	133	1	KV4B_HUMAN	P06313 homo sapien
35	388.5	59.3	108	1	KV5K_MOUSE	P01644 mus musculu
36	388.5	59.3	134	1	KV4C_HUMAN	P06314 homo sapien
37	386.5	59.0	136	1	KV5B_MOUSE	P01648 mus musculu
38	385.5	58.9	108	1	KV5O_MOUSE	P01648 mus musculu
39	384	58.6	129	1	KV3L_HUMAN	P18135 homo sapien
40	383.5	58.5	108	1	KV5L_MOUSE	P01645 mus musculu
41	383.5	58.5	108	1	KV5M_MOUSE	P01646 mus musculu
42	383.5	58.5	108	1	KV5N_MOUSE	P01647 mus musculu
43	383.5	58.5	149	1	KV5A_MOUSE	P01633 mus musculu
44	381	58.2	129	1	KV3M_HUMAN	P18136 homo sapien
45	379	57.9	107	1	KV6A_MOUSE	P01675 mus musculu

ALIGNMENTS

RESULT 1	ID	KV4A_MOUSE	STANDARD;	PRT;	129 AA.
AC	P01680;				
DT	21-JUL-1966 (Rel. 01, Created)				
DT	21-JUL-1966 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig kappa chain V-IV region S107B precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxId=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=82115300; PubMed=6799208;				
RA	Kwan S.-P., Max B.R., Seidman J.G., Leder P., Scharff M.D.;				
RT	"Two kappa immunoglobulin genes are expressed in the myeloma S107. ";				
RL	Cell 26:57-66(1981).				
CC	-I- MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO				
CC	AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS				
CC	SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE				
CC	NORMAL KAPPA CHAIN S107.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
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CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; J00577; AAA8780.1; -				
DR	EMBL; V00780; CAA24157.1; -				
DR	PIR; A01943; KWA57B.				
DR	HSSP; P01679; 2PB1.				
DR	InterPro; IPR007110; Ig_1like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_V.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS50835; IG_LIKE; 1.				
KM	Immunoglobulin V region; Signal.				
FT	SIGNAL	1	22		
FT	CHAIN	23	129		IG KAPPA CHAIN V-IV REGION S107B.
FT	DOMAIN	23	45		FRAMEWORK-1.
FT	DOMAIN	46	57		COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	58	72		FRAMEWORK-2.
FT	DOMAIN	73	79		COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	80	111		FRAMEWORK-3.
FT	DOMAIN	112	118		COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	119	128		FRAMEWORK-4.
FT	DISULFID	45	111		BY SIMILARITY.
FT	NON TER	129	129		
SO	SEQUENCE	129 AA;	13833 MW;	E4BB73072DC6B84 CRC64;	

Query Match

68.1%; Score 446; DB 1; Length 129;

Best Local Similarity 66.9%; Pred. No. 3.5e-36;
Matches 87; Conservative 21; Mismatches 18; Indels 4; Gaps 2;

QY 1 MPOVOIFSEFLISAVISVIRSDICMTQSPSSLSASVGRVITTCATSSI--TMSWYQ 58
DB 1 MLQVOVITLIVLSTVLSVSKGENVLTQSPALMAASLQKVTMTCSASSVSSYLHWYQ 60
QY 59 QKPGKAPKLLIYDTSNMGASVSPFSGSGGTDYTLTISLQPEDPATYTCQOMSSYP 118
DB 61 QKSGASPKLIRHTSLASGVAPRPFSGSGGTSYSLTISVLAEDDATTYTCQOMSGYF-- 118
QY 119 FGGGTKEIK 128
DB 119 FGGGTKEIK 128

RESULT 2

KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DS Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hillechmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.)";
RL Hope-Sejler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hillechmann N., Barnikol H.U., Hesse M., Langer B., Ponetjngl H.,
RA Stejmetz-Kayne M., Suter L., Watanabe S.;
RL (In) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCR-JONES PROTEIN.
CC PIR: A91638; KIHURY.
DR HSSP; P80362; IWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003006; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDS5A313DF3A CRC64;

Query Match 67.9%; Score 444.5; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 4e-36;
Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPKAPKLLIYDTSNMGASVPS 81

DB 1 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPKAPKLLIYDTSNMGASVPS 81

QY 82 RFGSGSGTDYTLTISLQPEDPATYTCQOMSSYP 128
DB 61 RFGSGSGTDYTLTISLQPEDPATYTCQOMSSYP 107

RESULT 3

KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DS Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwalet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; KIHUBN.
DR HSSP; P80362; IWTU.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003006; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Amyloid.

FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 67.4%; Score 441.5; DB 1; Length 108;
Best Local Similarity 78.5%; Pred. No. 7.7e-36;
Matches 84; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 23 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPKAPKLLIYDTSNMGASVPS 81
DB 1 DIQMTQSPSSLSASVGRVITTCATSSIT-YMSWYQKPKAPKLLIYDTSNMGASVPS 60

QY 82 RFGSGSGTDYTLTISLQPEDPATYTCQOMSSYP 128
DB 61 RFGSGSGTDYTLTISLQPEDPATYTCQOMSSYP 107

RESULT 4

KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DS Ig kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:33:29 ; Search time 21.8093 Seconds

(without alignments)
1514.523 Million cells updates/sec

Title: US-09-772-103-8

Perfect score: 655
Sequence: 1 MDPVQVIFSLISAVILS.....COQMSYPLTRGGKRVK 128

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL.23:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioid:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510	77.9	134	11	Q8VDD0
2	477	72.8	235	11	Q91W12
3	448	68.4	107	4	Q96SA9
4	436.5	66.6	108	4	Q9UL77
5	428.5	65.4	108	4	Q9UL70
6	417	63.7	107	4	Q9UL81
7	415	63.4	112	11	Q8K1F3
8	413	63.1	112	11	Q8K1F2
9	411	62.7	106	5	Q9U410
10	410.5	62.7	108	4	Q9UL79
11	405.5	61.9	234	11	Q8R062
12	403.5	61.6	233	11	Q91WS9
13	397	60.6	112	11	Q8K1F0
14	397	60.6	114	11	Q8K1F1
15	396.5	60.5	116	4	Q96PF6
16	395.5	60.4	109	11	Q920E6

ALIGNMENTS

17	387.5	59.2	234	11	Q8VCP0	Q8VCP0 mus musculu
18	387.5	59.2	298	11	Q9QIF0	Q9QIF0 mus musculu
19	387	59.1	109	4	Q9UL78	Q9UL78 homo sapien
20	386.5	59.0	107	11	Q9JL84	Q9JL84 mus musculu
21	379.5	57.9	214	11	Q9JL85	Q9JL85 mus musculu
22	375.5	57.3	234	11	Q9JL78	Q9JL78 mus musculu
23	375	57.3	109	4	Q9JL85	Q9JL85 mus musculu
24	372.5	56.9	97	11	Q9JL76	Q9JL76 mus musculu
25	370.5	56.4	234	4	Q8NEK1	Q8NEK1 mus musculu
26	369.5	56.4	108	11	Q8VJ30	Q8VJ30 mus musculu
27	364.5	55.6	108	4	Q9UL83	Q9UL83 homo sapien
28	363.5	55.5	111	11	Q920E9	Q920E9 mus musculu
29	361.5	55.2	101	11	Q9JL78	Q9JL78 mus musculu
30	361	55.1	109	4	Q9UL86	Q9UL86 mus musculu
31	357.5	54.6	127	11	Q925S9	Q925S9 mus musculu
32	341	52.1	238	11	Q9PM37	Q9PM37 mus musculu
33	337	51.5	238	11	Q8VCI6	Q8VCI6 mus musculu
34	337	51.5	239	11	Q8VCS5	Q8VCS5 mus musculu
35	328	50.1	239	4	Q8NEK0	Q8NEK0 mus musculu
36	328.5	49.8	107	11	Q9ER29	Q9ER29 mus musculu
37	324	49.5	239	4	Q8TCD0	Q8TCD0 mus musculu
38	324	49.5	241	11	Q921A6	Q921A6 mus musculu
39	321.5	49.1	99	11	Q9JL74	Q9JL74 mus musculu
40	319.5	48.8	103	11	Q9JL80	Q9JL80 mus musculu
41	319.5	48.8	239	11	Q8K0F8	Q8K0F8 mus musculu
42	310.5	47.4	234	11	Q8R028	Q8R028 mus musculu
43	309	47.2	104	11	Q9JL82	Q9JL82 mus musculu
44	297.5	45.4	114	4	Q9JL80	Q9JL80 mus musculu
45	294.5	45.0	109	6	Q9N0W5	Q9N0W5 oryctolagus

RESULT 1

Q8VDD0 ID Q8VDD0 PRELIMINARY; PRT; 134 AA.
AC Q8VDD0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anti-MOG 212 variable light chain (Fragment).
GN ANTI-MOG KAPPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chernajovsky Y.i;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Sembl P.i;
RT "Targeting T cells to the CNS."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ416311; CAC94866.1; -
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14525 MW; CFP8E2236B2DOCF CRC64;

Query Match 77.9%; Score 510; DB 11; Length 134;
Best Local Similarity 77.3%; Pred. No. 4.9e-44;

Matches 99; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

Oy 1 MDPVQVIFSLISAVILSRGDIQMTQSPSSLSASVGRVITTCATSSITYSWYQOK 60

```

Db 1 MDPQVQIFSLISAVLSRQIVLTQSPALMSAPGKVTMTCSASSISYMHMYQOK 60
Qy 61 PGKAPKLLIYDTSNLSAGVPSRFSGSGGTDTLTISLQPEDPATYTCQWSSYPLTFG 120
Db 61 POTSFKRWIYDTSKLSAGVPAPRFSGSGGTSTSLTISNMEADATYTCQWSSYPLTFG 120
Qy 121 GGTKEIK 128
Db 121 GGTKEIK 128

```

RESULT 2

Q91W12 PRELIMINARY; PRT; 235 AA.

```

AC 091W12;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DB Unknown (Protein for MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AA006643.1; -.
DR InterPro; IPR007110; I9_1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_v.
DR Pfam; PF00047; I9; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; I9_LIKE; 2.
DR PROSITE; PS00290; I9_MHC; 1.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDBD5B8FEF CRC64;

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Query Match 72.8%; Score 477; DB 11; Length 235;
 Best Local Similarity 71.1%; Pred. No. 2,2e-40;
 Matches 91; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

```

Qy 1 MDPQVQIFSLISAVLSRQIVLTQSPALMSAPGKVTMTCSASSISYMHMYQOK 60
Db 1 MDPQVQIFSLISAVLSRQIVLTQSPALMSAPGKVTMTCSASSISYMHMYQOK 60
Qy 61 PGKAPKLLIYDTSNLSAGVPSRFSGSGGTDTLTISLQPEDPATYTCQWSSYPLTFG 120
Db 61 POTSFKRWIYDTSKLSAGVPAPRFSGSGGTSTSLTISNMEADATYTCQWSSYPLTFG 120
Qy 121 GGTKEIK 128
Db 121 GGTKEIK 128

```

RESULT 3

Q96SA9 PRELIMINARY; PRT; 107 AA.

```

AC 096SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DB Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain
variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98375693; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;

```

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RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AB68785.1; -.
DR InterPro; IPR007110; I9_1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_v.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; I9_LIKE; 1.
FT NON_TER 107
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43B9C5B577F16 CRC64;

```

Query Match 68.4%; Score 448; DB 4; Length 107;
 Best Local Similarity 85.0%; Pred. No. 7.2e-38;
 Matches 91; Conservative 6; Mismatches 8; Indels 2; Gaps 2;

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Qy 23 DIQMTQSPSSLSASVGRVTTCATSSSI-TYMSWYQOKPGKAPKLLIYDTSNLSAGVPS 81
Db 1 DIQMTQSPSSLSASVGRVTTCATSSISYLMWYQOKPGKAPKLLIYDTSNLSAGVPS 60
Qy 82 RFSGSGGTDTLTISLQPEDPATYTCQWSSYPLTFGSGTKEIK 128
Db 61 RFSGSGGTDTLTISLQPEDPATYTCQWSSYPLTFGSGTKEIK 106

```

RESULT 4

Q9UL77 PRELIMINARY; PRT; 108 AA.

```

AC 09UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DB Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Betney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; I9_1like.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_v.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; I9_LIKE; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716CAD16F3 CRC64;

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Query Match 66.6%; Score 436.5; DB 4; Length 108;
 Best Local Similarity 82.2%; Pred. No. 1.1e-36;
 Matches 88; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

```

Qy 23 DIQMTQSPSSLSASVGRVTTCATSSSI-TYMSWYQOKPGKAPKLLIYDTSNLSAGVPS 81
Db 1 DIQMTQSPSSLSASVGRVTTCATSSISYLMWYQOKPGKAPKLLIYDTSNLSAGVPS 60
Qy 82 RFSGSGGTDTLTISLQPEDPATYTCQWSSYPLTFGSGTKEIK 128
Db 61 RFSGSGGTDTLTISLQPEDPATYTCQWSSYPLTFGSGTKEIK 107

```

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:09 : Search time 27.2617 Seconds
(without alignments)
745.259 Million cell updates/sec

Title: US-09-772-103-8
Sequence: 1 MDPQVGFSLISASVILS.....CQMSYPLFGGTVEIK 128
Perfect score: 655

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	655	100.0	128	22	AA66522
2	609	93.0	128	17	AAR90684
3	600	91.6	128	21	AAV77597
4	600	91.6	128	22	AAV78866
5	599	91.5	235	18	AAW41398
6	593	90.5	235	15	AAW41411
7	590	90.1	133	15	AAR53345
8	590	90.1	133	20	AAV28394
9	590	90.1	133	20	AAV28371

10	587	89.6	126	21	AAV77599	Anti-human VEGF re
11	587	89.6	126	22	AAV78868	Anti-human Flt-1 a
12	584	89.2	130	19	AAW73179	Fragment of gangli
13	584	89.2	130	19	AAW73180	Fragment of gangli
14	584	89.2	130	20	AAV28375	Human chimeric ant
15	584	89.2	130	20	AAV28376	Human chimeric ant
16	583	89.0	235	18	AAW41410	Humanised light ch
17	580	88.5	130	20	AAW73181	Fragment of gangli
18	580	88.5	130	20	AAV28377	Human chimeric ant
19	573	87.5	126	21	AAV77601	Anti-human VEGF re
20	573	87.5	126	22	AAV78870	Anti-human Flt-1 a
21	572	87.3	130	19	AAW73182	Fragment of gangli
22	572	87.3	130	20	AAV28378	Human chimeric ant
23	571	87.2	130	19	AAW73185	Fragment of gangli
24	571	87.2	130	20	AAV28381	Human chimeric ant
25	568	86.7	130	19	AAW73184	Fragment of gangli
26	568	86.7	130	20	AAV28380	Human chimeric ant
27	567	86.6	130	19	AAV73173	Light chain of gan
28	567	86.6	130	20	AAV28382	Human chimeric ant
29	566	86.4	130	21	AAV07970	A light chain vari
30	564	86.1	130	19	AAW73176	Fragment of gangli
31	562	85.8	130	19	AAW73183	Human chimeric ant
32	562	85.8	130	20	AAV28379	Fragment of gangli
33	560	85.5	130	19	AAW73174	Human chimeric ant
34	560	85.5	130	20	AAV28383	Light chain of gan
35	543	82.9	235	17	AAW06180	Human chimeric ant
36	528	80.6	128	22	AA66521	Humanised A5B57 11
37	523	79.8	235	18	AAW41392	Mouse antibody 26
38	520	79.4	126	21	AAV77598	Chimeric anti-CRA
39	520	79.4	126	22	AAV78867	Anti-human VEGF re
40	520	79.4	128	13	AAR27050	Anti-human Flt-1 a
41	519	79.2	128	22	AAV69655	V425 antibody c10
42	518	79.1	126	19	AAW36164	Murine mAb-beta1 a
43	517	78.9	128	12	AAR13227	Humanised light ch
44	516	78.8	129	17	AAR88108	Light (kappa) chai
45	514	78.5	128	17	AAR90690	Murine anti-Protein

ALIGNMENTS

RESULT 1	AA66522	AA66522 standard; Protein; 128 AA.
ID	AA66522;	
AC	AA66522;	
XX		
22-OCT-2001	(first entry)	
DT		
XX		
DE	Humanised anti-CTLA4 light chain.	
XX		
XX		
Human: CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;		
immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;		
T cell; humanised antibody; autoimmune disorder; graft rejection;		
allergy; light chain.		
XX		
OS	Homo sapiens.	
OS	Mus musculus.	
OS	Synthetic.	
XX		
PN	WO200154732-A1.	
XX		
PD	02-AUG-2001.	
XX		
PF	26-JAN-2001; 2001WO-US02653.	
XX		
PR	27-JAN-2000; 2000US-0178473.	
XX		
PA	(GENY) GENETICS INST INC.	
XX		
PI	Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;	
PI	O'Hara D, Hinton P, Tsurushita N;	
XX		

DR MPI: 2001-483195/52.
N-PSDB; AAH76440, AAH76442.

PT Novel antibody-toxic group conjugate comprising an antibody that specifically recognizes a molecule expressed only on activated T cells, useful for recognizing a molecule expressed only on activated T cells, useful for modulating immune response for treating autoimmune disorder, allergic response

XX Claim 14; Fig 9; 123pp; English.

CC The invention relates to an antibody-toxic group conjugate comprising an antibody that specifically recognizes a molecule expressed only on activated T cells, and a toxic group. The T cell molecule is preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4). The antibody of the invention is a humanised anti-CTLA4 antibody comprising a sequence of 128 or 142 amino acids fully defined in the specification. The antibody-toxic group conjugate is useful for modulating the immune response in a subject suffering from a disorder or condition such as autoimmune disorder, immune response to a graft, allergic response or an immune response to a therapeutic protein. The antibody is also useful for research purposes, e.g., in staining and isolating CTLA4-bearing cells. The antibody is also useful for T-cell typing, for isolating specific IL-2 receptor-bearing cells or fragments of the receptor, for vaccine preparation, and for determining the effectiveness of an agent to down-regulate CTLA4 activity. The present sequence is the light chain of humanised anti-CTLA4 antibody.

CC Sequence 128 AA:

Query Match 100.0%; Score 655; DB 22; Length 128;
Best Local Similarity 100.0%; Pred. No. 2,3e-41;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPVOIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCSATSSITVMSWYQOK 60
DB 1 MDPVOIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCSATSSITVMSWYQOK 60
QY 61 PGKAPKLLIYDTSNMLASGVSRPFGSGSGTDYTLTISLSQPEDPATYTCQOMSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNMLASGVSRPFGSGSGTDYTLTISLSQPEDPATYTCQOMSSYPLTFG 120
QY 121 GGTVEIK 128
DB 121 GGTVEIK 128

RESULT 2
AAR90684
ID AAR90684 standard; protein; 128 AA.

AC AAR90684;
DT 16-AUG-1996 (first entry)

DE Humanized 5C7.29 antibody light chain variable region.

KW Humanized 5C7.29 antibody light chain variable region;
KW P-selectin binding agent; P-selectin binding agent; diagnosis;
KW therapy; inflammation; ischaemia-reperfusion injury; trauma;
KW adult respiratory distress syndrome; stroke; sepsis; psoriasis;
KW autoimmune disease; affinity purification; drug screening;
KW anti-idiotypic antibody generation.

OS Synthetic.

PH Key Location/Qualifiers

FT Protein 23..128

FT Region /note= "humanized antibody mature light chain"

FT Region /note= "complementarity determining region"

FT Region /note= "complementarity determining region"

FT Region 110..118
FT /note= "complementarity determining region"

XX MO9534324-A1.

XX 21-DEC-1995.

XX 07-JUN-1995; 95WO-US07302.

XX 14-JUN-1994; 94US-0259963.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Berg EL;

XX MPI: 1996-049423/05.

XX N-PSDB; AAT15537.

PT Monoclonal and humanised antibodies having specificity for P- and E-selectin - useful for treatment of inflammatory diseases, e.g. ischaemia-reperfusion injury, psoriasis, etc.

PS Claim 13; Fig 8a; 89pp; English.

CC This humanized 5C7.29 antibody light chain variable region, together with the corresponding heavy chain variable region (see AAR90685), results in a humanized antibody that specifically binds to P- and E-selectin and inhibits the binding of selectins to a counterreceptor of the selectins. The humanized light chain variable region contains complementarity determining regions (CDRs) having amino acid sequences from non-human antibody light chain and consists of a variable region framework sequence substantially identical to a human light chain variable region framework sequence. The humanized antibody may be used in the diagnosis and therapy of inflammation and conditions such as ischaemia-reperfusion injury, adult respiratory distress syndrome, trauma, stroke, sepsis, psoriasis and autoimmune disease. It may also be used in affinity purification of selectin and cells, generation of anti-idiotypic antibodies, and in the screening of therapeutic agents having the same binding specificity as a cross-reacting antibody.

CC Sequence 128 AA:

Query Match 93.0%; Score 609; DB 17; Length 128;
Best Local Similarity 93.0%; Pred. No. 5.8e-36;
Matches 119; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDPVOIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCSATSSITVMSWYQOK 60
DB 1 MDPVOIFSFLLISAVILSRGDIQMTQSPSSLSASVGRVITTCSATSSITVMSWYQOK 60

QY 61 PGKAPKLLIYDTSNMLASGVSRPFGSGSGTDYTLTISLSQPEDPATYTCQOMSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNMLASGVSRPFGSGSGTDYTLTISLSQPEDPATYTCQOMSSYPLTFG 120

QY 121 GGTVEIK 128

DB 121 GGTVEIK 128

RESULT 3
AA77597
ID AA77597 standard; peptide; 128 AA.

XX AA77597;

XX 08-MAY-2000 (first entry)

DE Anti-human VEGF receptor Flt-1 antibody related peptide sequence #92.

KW Antibody; human; vascular endothelial growth factor; VEGF receptor;
KW Flt-1; neovascularisation; cell proliferation; metastasis; tumour;
KW rheumatoid arthritis; retinopathy; psoriasis.

1:21 2003

us-09-772-103-8.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:44:30 ; Search time 18.4341 Seconds
(without alignments)
1280.712 Million cell updates/sec

Title: US-09-772-103-8

Sequence: 1 MDPVOQIFSFLLISASVILS.....CQWSSYPLTFGGCTVEIK 128

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubppa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	600	91.6	128	15	US-10-160-232-92
2	599	91.5	235	15	US-09-910-059-52
3	593	90.5	235	10	US-09-910-059-99
4	587	89.6	126	15	US-10-160-232-94
5	583	89.0	235	10	US-09-910-059-97
6	573	87.5	126	15	US-10-160-232-96
7	567	86.6	130	15	US-10-160-232-96
8	564	86.1	130	15	US-10-195-752-111
9	563	79.8	235	10	US-09-910-059-17
10	520	79.4	126	15	US-10-160-232-93
11	514	78.5	233	15	US-10-071-485-69
12	500	76.3	110	9	US-09-753-436-96
13	500	76.3	110	12	US-10-163-942-96
14	499	76.2	107	10	US-09-910-059-50
15	496.5	75.8	258	15	US-10-207-655-343

16	496.5	75.8	492	15	US-10-207-655-344	Sequence 344, App
17	496.5	75.8	543	15	US-10-207-655-345	Sequence 345, App
18	496.5	75.8	543	15	US-10-207-655-346	Sequence 346, App
19	496	75.7	107	10	US-09-910-059-61	Sequence 61, App1
20	495	75.6	128	12	US-10-244-821-92	Sequence 92, App1
21	493	75.3	107	10	US-09-910-059-71	Sequence 71, App1
22	493	75.3	128	15	US-10-160-232-87	Sequence 87, App1
23	490	74.8	126	15	US-10-160-232-89	Sequence 89, App1
24	490	74.8	128	11	US-09-967-719C-6	Sequence 4, App11
25	490	74.8	128	11	US-09-967-719C-6	Sequence 6, App11
26	488	74.5	235	11	US-09-795-515-5	Sequence 3, App11
27	487	74.4	106	9	US-09-796-848A-3	Sequence 1, App11
28	487	74.4	106	10	US-09-771-415-17	Sequence 8, App11
29	487	74.4	107	15	US-10-267-286A-8	Sequence 256, App
30	487	74.4	131	15	US-10-207-655-256	Sequence 231, App
31	487	74.4	213	10	US-09-996-288-231	Sequence 231, App
32	487	74.4	213	11	US-09-996-285-231	Sequence 231, App
33	487	74.4	266	15	US-10-207-655-260	Sequence 260, App
34	487	74.4	550	15	US-10-207-655-270	Sequence 270, App
35	485	74.0	106	10	US-09-771-415-17	Sequence 16, App
36	485	74.0	106	12	US-10-127-850-165	Sequence 54, App1
37	484	73.9	106	11	US-09-996-285-54	Sequence 54, App1
38	484	73.9	106	11	US-09-996-285-54	Sequence 211, App
39	484	73.9	106	12	US-10-020-354-54	Sequence 211, App
40	484	73.9	213	10	US-09-996-288-211	Sequence 211, App
41	484	73.9	107	11	US-09-996-285-211	Sequence 65, App1
42	483	73.7	107	10	US-09-910-059-65	Sequence 65, App1
43	482	73.6	213	9	US-09-881-823-6	Sequence 255, App
44	482	73.6	213	10	US-09-996-288-255	Sequence 255, App
45	482	73.6	213	11	US-09-996-285-255	Sequence 255, App

ALIGNMENTS

RESULT 1
US-10-160-232-92
Sequence 92, Application US/10160232
Publication No. US20030088075A1
GENERAL INFORMATION:
APPLICANT: SHITTARA, KENYA
APPLICANT: ITO, MIKITO
APPLICANT: HANAI, NOBIO
APPLICANT: KAWADA, YOKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHIBUYA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
FILE REFERENCE: 249-107
CURRENT APPLICATION NUMBER: US/10/160,232
PRIOR FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 09/315,051
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/119,014
PRIOR FILING DATE: 1998-07-20
PRIOR APPLICATION NUMBER: PCT/JP97/04259
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 92
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-10-160-232-92
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Best Local Similarity 91.4%; Pred. No. 4e-44;
Matches 117; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Db 1 MDPVOVIFSFLLISASVILSRGDIQMTQSPSSLSASVGDGVITTCSSASSSVTHMYQOK 60
Qy 61 PGKAPKLLIYDTSNLASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
Db 61 PGKAPKLLIYDTSNLASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
Qy 121 GGTKEIK 128
Db 121 GGTKEIK 128
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RESULT 2

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US-09-910-059-52
; Sequence 52, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: complete humanised light chain sequence
US-09-910-059-52
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Best Local Similarity 91.4%; Pred. No. 9, 3e-44;
Matches 117; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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Db 1 MDPVOVIFSFLLISASVILSRGDIQMTQSPSSLSASVGDGVITTCSSASSSVTHMYQOK 60
Qy 61 PGKAPKLLIYDTSNLASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
Db 61 PGKAPKLLIYDTSNLASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
Qy 121 GGTKEIK 128
Db 121 GGTKEIK 128
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RESULT 3

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US-09-910-059-99
; Sequence 99, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; APPLICATION NUMBER: US/09/910,059
; DATE: 2001-07-23
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; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanised light chain Fd sequence
US-09-910-059-99
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Db 121 GGTKEIK 128
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RESULT 4

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US-10-160-232-94
; Sequence 94, Application US/10160232
; Publication No. US20030088075A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: ITO, MIKITO
; APPLICANT: HANAI, NOBUO
; APPLICANT: KAWADA, YOKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: SHIBUYA, MASABUMI
; TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTIBODY
; FILE REFERENCE: 249-107
; CURRENT APPLICATION NUMBER: US/10/160,232
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US/09/453,718
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 09/315,051
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/119,014
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: PCT/JP97/04259
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 94
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein
US-10-160-232-94
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Best Local Similarity 90.6%; Pred. No. 5.1e-43;
Matches 116; Conservative 5; Mismatches 5; Indels 2; Gaps 1;

Qy 1 MDPVOVIFSFLLISASVILSRGDIQMTQSPSSLSASVGDGVITTCSSASSSVTHMYQOK 60
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GenCore version 5.1.6
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OM protein - protein search, using bw model

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Title: US-09-772-103-8

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	590	90.1	133	2	US-08-438-562-37
7	590	90.1	133	2	US-08-483-528B-101
8	583	89.0	235	3	US-09-171-945-97
9	567	86.6	130	4	US-09-393-385B-111
10	564	86.1	130	4	US-09-393-385B-111
11	543	82.9	235	4	US-09-011-769A-27
12	520	79.4	128	1	US-07-946-421-26
13	519	79.2	128	1	US-07-634-278-31
14	519	79.2	128	1	US-08-477-728-31
15	519	79.2	128	1	US-08-474-040-31
16	519	79.2	128	1	US-08-487-200-31
17	519	79.2	128	1	US-08-484-537-31
18	518	79.1	126	2	US-08-656-586-6
19	518	79.1	126	2	US-09-171-945-17
20	516	78.8	129	5	PCT-US95-07302-12
21	514	78.5	128	3	US-08-619-491-2
22	514	78.5	128	3	PCT-US95-07302-2
23	514	78.5	233	4	US-09-485-737B-69
24	508	77.6	106	1	US-07-634-278-35
25	508	77.6	106	1	US-07-634-278-35
26	508	77.6	106	1	US-08-477-728-35
27	508	77.6	106	1	US-08-477-728-35

28	508	77.6	106	1	US-08-474-040-35	Sequence 35, Appl
29	508	77.6	106	1	US-08-474-040-35	Sequence 59, Appl
30	508	77.6	106	1	US-08-487-200-35	Sequence 35, Appl
31	508	77.6	106	1	US-08-487-200-35	Sequence 59, Appl
32	508	77.6	106	3	US-08-484-537-35	Sequence 35, Appl
33	508	77.6	106	3	US-08-484-537-35	Sequence 59, Appl
34	506	77.3	129	2	US-08-116-778E-2	Sequence 2, Appl
35	506	77.3	129	2	US-08-438-562-2	Sequence 92, Appl
36	506	77.3	129	2	US-08-483-528B-92	Sequence 8, Appl
37	503	76.8	106	3	US-08-397-411-12	Sequence 96, Appl
38	503	76.8	213	3	US-08-397-411-12	Sequence 96, Appl
39	500	76.3	110	1	US-08-482-882-96	Sequence 96, Appl
40	500	76.3	110	2	US-08-483-389-96	Sequence 96, Appl
41	500	76.3	110	2	US-08-487-113D-96	Sequence 96, Appl
42	500	76.3	110	2	US-08-473-503-96	Sequence 96, Appl
43	500	76.3	110	2	US-08-483-932-96	Sequence 96, Appl
44	500	76.3	110	2	US-08-720-420A-96	Sequence 96, Appl
45	500	76.3	110	3	US-08-714-017-96	Sequence 96, Appl

ALIGNMENTS

```

RESULT 1
US-08-619-491-6
; Sequence 6, Application US/08619491
; Patent No. 6210670
; GENERAL INFORMATION:
; APPLICANT: Berg, Ellen L.
; TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
; TITLE OF INVENTION: Specific for E-Selectin and P-Selectin
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/619,491
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/07302
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,963
; FILING DATE: 14-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 011823-005810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-619-491-6
; Query Match 93.0%; Score 609; DB 3; Length 128;
; Best Local Similarity 93.0%; Pred. No. 5,1e+46;
; Matches 119; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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QY 1 MDPVOVIFSFLLISASVILSRGDIOMTQSPSSLSASVGDRTVITTSATSSITVMSWYQOK 60
DB 1 MDPVOVIFSFLLISASVILSRGDIOMTQSPSSLSASVGDRTVITTSATSSITVMSWYQOK 60
QY 61 PKAPKLLIYDTSNLSASGVPSRFSGSGGTDTYTLTISLQPEDPATYTCQOMSSYPLTFPG 120
DB 61 PKAPKLLIYDTSNLSASGVPSRFSGSGGTDTYTLTISLQPEDPATYTCQOMSSYPLTFPG 120
QY 121 GGTKEVEIK 128
DB 121 GGTKEVEIK 128

RESULT 2

PCT-US95-07302-6
Sequence 6, Application PC/TUS9507302
GENERAL INFORMATION:
APPLICANT: Berg, Ellen L.
TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
TITLE OF INVENTION: Specific for E-Selectin and P-Selectin
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: PCT/US95/07302
APPLICATION NUMBER: PCT/US95/07302
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/259,963
FILING DATE: 14-JUNE-94
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-005810PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07302-6

Query Match 93.0%; Score 609; DB 5; Length 128;
Best Local Similarity 93.0%; Pred. No. 5, 1e-48;
Matches 119; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDPVOVIFSFLLISASVILSRGDIOMTQSPSSLSASVGDRTVITTSATSSITVMSWYQOK 60
DB 1 MDPVOVIFSFLLISASVILSRGDIOMTQSPSSLSASVGDRTVITTSATSSITVMSWYQOK 60
QY 61 PKAPKLLIYDTSNLSASGVPSRFSGSGGTDTYTLTISLQPEDPATYTCQOMSSYPLTFPG 120
DB 61 PKAPKLLIYDTSNLSASGVPSRFSGSGGTDTYTLTISLQPEDPATYTCQOMSSYPLTFPG 120
QY 121 GGTKEVEIK 128
DB 121 GGTKEVEIK 128

RESULT 3

US-09-171-945-52
Sequence 52, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 52
LENGTH: 235
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-52

Query Match 91.5%; Score 599; DB 3; Length 235;
Best Local Similarity 91.4%; Pred. No. 8, 1e-47;
Matches 117; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDPVOVIFSFLLISASVILSRGDIOMTQSPSSLSASVGDRTVITTSATSSITVMSWYQOK 60
DB 1 MDPVOVIFSFLLISASVILSRGDIOMTQSPSSLSASVGDRTVITTSATSSITVMSWYQOK 60
QY 61 PKAPKLLIYDTSNLSASGVPSRFSGSGGTDTYTLTISLQPEDPATYTCQOMSSYPLTFPG 120
DB 61 PKAPKLLIYDTSNLSASGVPSRFSGSGGTDTYTLTISLQPEDPATYTCQOMSSYPLTFPG 120
QY 121 GGTKEVEIK 128
DB 121 GGTKEVEIK 128

RESULT 4

US-09-171-945-99
Sequence 99, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 99
LENGTH: 235
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-99

Query Match 90.5%; Score 593; DB 3; Length 235;
Best Local Similarity 90.6%; Pred. No. 2.8e-46;
Matches 116; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDPVOIFSPFLILASVILSRGDIOMTOSPSLSASVGRVITTCASITTSITMSWYOOK 60
DB 1 MDPVOIFSPFLILASVILSRGDIOMTOSPSLSASVGRVITTCASITTSITMSWYOOK 60
QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTITSLQPEDPATYTCQOQSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTITSLQPEDPATYTCQOQSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 5

US-08-116-778E-37
; Sequence 37, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUMANA, YOSHIOHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYTE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-116-778E-37

Query Match 90.1%; Score 590; DB 2; Length 133;
Best Local Similarity 89.8%; Pred. No. 2.8e-46;
Matches 115; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDPVOIFSPFLILASVILSRGDIOMTOSPSLSASVGRVITTCASITTSITMSWYOOK 60
DB 1 MDPVOIFSPFLILASVILSRGDIOMTOSPSLSASVGRVITTCASITTSITMSWYOOK 60
QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTITSLQPEDPATYTCQOQSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTITSLQPEDPATYTCQOQSSYPLTFG 120

QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 6

US-08-438-562-37
; Sequence 37, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUMANA, YOSHIOHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYTE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-438-562-37

Query Match 90.1%; Score 590; DB 2; Length 133;
Best Local Similarity 89.8%; Pred. No. 2.8e-46;
Matches 115; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDPVOIFSPFLILASVILSRGDIOMTOSPSLSASVGRVITTCASITTSITMSWYOOK 60
DB 1 MDPVOIFSPFLILASVILSRGDIOMTOSPSLSASVGRVITTCASITTSITMSWYOOK 60
QY 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTITSLQPEDPATYTCQOQSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPSRFGSGSGTDYTLTITSLQPEDPATYTCQOQSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 7
US-08-483-528B-101

Sequence 101, Application US/084835288
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHIOHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-528B-101

Query Match 90.1%; Score 590; DB 2; Length 133;
Best Local Similarity 89.8%; Pred. No. 2.8e-46;
Matches 115; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDFOVQIFSFLLISASVLSRGDIQMTQSPSSLSASVGDRTVITCSATSSITVMSWYQOK 60
DB 1 MHFOVQIFSFLLISASVLSRGDIQMTQSPSSLSASVGDRTVITCSATSSITVMSWYQOK 60

QY 61 PGKAPKLLIYDTSNLASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120

QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 8
US-09-171-945-97
Sequence 97, Application US/09171945
Patent No. 6277599
GENERAL INFORMATION:
APPLICANT: Emery, Stephen
APPLICANT: Copley, Clive Graham
APPLICANT: Edge, Michael Derek
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
FILE REFERENCE: Monoclonal Antibody to CEA
CURRENT APPLICATION NUMBER: US/09/171,945
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: GB9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
PRIOR APPLICATION NUMBER: PCT/GB97/01165

PRIOR FILING DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 97
LENGTH: 235
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-97

Query Match 89.0%; Score 583; DB 3; Length 235;
Best Local Similarity 89.1%; Pred. No. 2.2e-45;
Matches 114; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDFOVQIFSFLLISASVLSRGDIQMTQSPSSLSASVGDRTVITCSATSSITVMSWYQOK 60
DB 1 MHFOVQIFSFLLISASVLSRGDIQMTQSPSSLSASVGDRTVITCSATSSITVMSWYQOK 60

QY 61 PGKAPKLLIYDTSNLASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPSRFSGSGGTDYTLTISLQPEDPATYTCQOMSSYPLTFG 120

QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 9
US-09-393-385B-111
Sequence 111, Application US/09393385B
Patent No. 6423511
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHIOHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-393-385B-111

Query Match 86.6%; Score 567; DB 4; Length 130;
Best Local Similarity 86.7%; Pred. No. 3.2e-44;
Matches 111; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Tue Dec 2 07:01:20 2003

us-09-772-103-8.ra1

Page 5

[illegible]

RESULT 10
US-09-393-385B-113

Sequence 113, Application US/09393385B
Patent No. 6423511
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHIIISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-6714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Releasee #1.0, Version #1.25B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,385B
FILING DATE: 27-JUN-96
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: protein
IS-09-393-385B-113

Query Match	86.1%;	Score 564;	DB 4;	Length 130;
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[illegible]

RESULT 11
US-09-011-769A-27

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: Sequence 27, Application US/09011769A
: Patent No. 6436691
:
: GENERAL INFORMATION:
: APPLICANT: SLATER, Anthony M.
:          BLAKER, David C.
:          DAVIES, David H.
:          HENNAM, John F.
:          HENNEQUIN, Laurent F.A.
:          MARSHAW, Peter R.
:          DOWELL, Robert I.
:
: TITLE OF INVENTION: Chemical Compounds
: NUMBER OF SEQUENCES: 87
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Pillsbury Madison & Sutro, LLP
: STREET: 1100 New York Ave., N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 1.44 Mb disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS Word
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/011,769A
: FILING DATE: 13-Feb-1998
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/GB96/01975
: FILING DATE: 13-AUG-1996
: APPLICATION NUMBER: GB 9612295.7
: FILING DATE: 12-JUN-1996
: APPLICATION NUMBER: GB 9611019.2
: FILING DATE: 25-MAY-1996
: APPLICATION NUMBER: GB 9516810.0
: FILING DATE: 16-AUG-1995
:
: INFORMATION FOR SEQ ID NO: 27:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 235 amino acids
:   TYPE: amino acid
:   TOPOLOGY: linear
:
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 27:
:
: US-09-011-769A-27

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Query Match	82.9%;	Score 543;	DB 4;	Length 235;
Best Local Similarity	82.8%;	Pred. No. 9.1e-42;		
Matches 106; Conservative	7;	Mismatches 15;	Indels 0;	Gaps 0;

QY	1	MPOVAVIPEFLLISASVILSRGDIOMTOSPSLSASVDRTYTTCASSTITYNMSWQOK	60
Dd	1	MFOVOVIFSFLLISASVIMSRGQTALITOSPSSLASVGDRTVTMCRASSSVTYTHMYQOK	60
QY	61	PGKAPRLTIIDYTSNLASGVSPRFSGSAGSGTDTLTTLISLOPEDFATYYYCOOWMSPTLFG	120
Dd	61	PGLAPRSMTIYANSLNASGVSPRFSGSAGSDTDTLTTLISLOPEDIAITYYCCQMWSKPFTFG	120
QY	121	GGTKVEIK	128
Dd	121	QGTRVEVK	128

RESULT 12
US-07-946-421-26
; Sequence 26, Application US/07946421

Patent No. 5558864
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Kettleborough, Catherine A.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,421
FILING DATE: 06-NOV-1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 911933892
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: Merck 1430
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-07-946-421-26

Query Match 79.4%; Score 520; DB 1; Length 128;
Best Local Similarity 77.3%; Pred. No. 5.4e-40;
Matches 99; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 1 MDPVOVIFSFLLISASVILSRGDIQMTGSPSSLSASVGDRTTTCATSSITTMWYQK 60
DB 1 MDPVOVIFSFLLISASVILSRGDIQMTGSPSSLSASVGDRTTTCATSSITTMWYQK 60
QY 61 PGKAPKLLIYDTSNLASGVPRFSGSGSGTDYTLTISLSQPEDPATYTCQWSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPRFSGSGSGTDYTLTISLSQPEDPATYTCQWSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 13
US-07-634-278-31
Sequence 31, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California

COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-31

Query Match 79.2%; Score 519; DB 1; Length 128;
Best Local Similarity 75.0%; Pred. No. 6.7e-40;
Matches 96; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MDPVOVIFSFLLISASVILSRGDIQMTGSPSSLSASVGDRTTTCATSSITTMWYQK 60
DB 1 MDPVOVIFSFLLISASVILSRGDIQMTGSPSSLSASVGDRTTTCATSSITTMWYQK 60
QY 61 PGKAPKLLIYDTSNLASGVPRFSGSGSGTDYTLTISLSQPEDPATYTCQWSSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLASGVPRFSGSGSGTDYTLTISLSQPEDPATYTCQWSSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 GGTKEIK 128

RESULT 14
US-08-477-728-31
Sequence 31, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-728-31

Query Match 79.2%; Score 519; DB 1; Length 128;
Best Local Similarity 75.0%; Pred. No. 6.7e-40;
Matches 96; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MFOVOIFSFLLISAVILSRGDIOMTOSPSLSASVGRVITTSATSSITMYWYOOK 60
DB 1 MFOVOIFSFLLISAVILSRGDIOMTOSPSLSASVGRVITTSATSSITMYWYOOK 60
QY 61 PGKAPKLLIYDTSNLSASVPSRFSGSGTDYTLTISLQPEDFATYCCOQMSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLSASVPSRFSGSGTDYTLTISLQPEDFATYCCOQMSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 AGTKLELK 128

RESULT 15
US-08-474-040-31
Sequence 31, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-040-31

Query Match 79.2%; Score 519; DB 1; Length 128;
Best Local Similarity 75.0%; Pred. No. 6.7e-40;
Matches 96; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MFOVOIFSFLLISAVILSRGDIOMTOSPSLSASVGRVITTSATSSITMYWYOOK 60
DB 1 MFOVOIFSFLLISAVILSRGDIOMTOSPSLSASVGRVITTSATSSITMYWYOOK 60
QY 61 PGKAPKLLIYDTSNLSASVPSRFSGSGTDYTLTISLQPEDFATYCCOQMSYPLTFG 120
DB 61 PGKAPKLLIYDTSNLSASVPSRFSGSGTDYTLTISLQPEDFATYCCOQMSYPLTFG 120
QY 121 GGTKEIK 128
DB 121 AGTKLELK 128

Search completed: December 2, 2003, 06:46:01
Job time: 10.8661 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:39:15 ; Search time 10.0811 Seconds

(Without alignments)
1354.605 Million cell updates/sec

Title: US-09-772-103-10

Perfect score: 742

Sequence: 1 MAVLVPLCLVAFPSCTL50.....MKRGYANDYWGQGLTVTVSS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 76: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	79.3	141	2	S52446 Ig heavy chain V r
2	561.5	75.7	139	2	A32456 Ig heavy chain V r
3	558	75.2	140	2	S55028 Ig heavy chain V r
4	528.5	71.2	135	2	S31913 Ig gamma-2A chain
5	525	70.8	117	2	S10111 Ig gamma-1 chain V r
6	510	68.7	140	2	S14238 Ig gamma-1 chain p
7	506	68.2	144	1	G2MS14 Ig heavy chain pre
8	504.5	68.0	144	2	S11244 Ig gamma-2a chain
9	491	66.2	140	2	I37782 Ig variable region
10	483.5	65.2	137	2	S31676 Ig heavy chain V r
11	481.5	64.9	139	2	PL0087 Ig heavy chain V r
12	481.5	64.9	139	2	S31586 Ig heavy chain V r
13	478	64.4	116	2	A33932 Ig mu chain precu
14	478	64.4	155	2	S31511 Ig heavy chain - h
15	476	64.2	147	2	S13519 Ig heavy chain V r
16	475	64.0	116	1	G1MS10 Ig heavy chain pre
17	475	63.2	112	2	S31512 Ig heavy chain - h
18	469	63.0	145	2	S78055 Ig heavy chain pre
19	467.5	63.0	145	2	S78055 Ig heavy chain pre
20	467	62.9	130	2	S31590 Ig heavy chain V r
21	466	62.8	114	2	S11106 Ig heavy chain V r
22	464	62.5	113	2	S11101 Ig heavy chain V r
23	464	62.5	115	1	HVMS14 Ig heavy chain pre
24	464	62.5	116	2	S11102 Ig heavy chain V r
25	464	62.5	127	2	B31807 Ig heavy chain V r
26	459	61.9	146	2	S09711 Ig heavy chain V r
27	458	61.7	118	2	P00266 Ig heavy chain V r
28	456.5	61.5	117	2	S38563 Ig heavy chain V r
29	456	61.5	146	2	S09710 Ig heavy chain V r

30	454	61.2	139	2	S31596	Ig heavy chain V r
31	453	61.1	140	2	A49045	Ig heavy chain V r
32	450.5	60.7	116	2	S42484	Ig heavy chain V r
33	449	60.5	114	2	S11099	Ig heavy chain V r
34	449	60.5	115	2	S11103	Ig heavy chain V r
35	447	60.2	106	2	S26322	Ig heavy chain V r
36	447	60.2	112	2	S11108	Ig heavy chain V r
37	446	60.1	135	2	S78051	Ig heavy chain V r
38	444.5	59.9	118	2	S32786	Ig heavy chain pre
39	444	59.8	121	2	S33131	Ig heavy chain (an
40	442.5	59.6	140	2	S78052	Ig heavy chain V r
41	441	59.4	114	2	S26321	Ig heavy chain pre
42	441	59.4	140	2	S54239	Ig mu heavy chain
43	441	59.4	144	2	S54244	Ig mu heavy chain
44	439	59.2	121	2	D30560	Ig heavy chain V r
45	438.5	59.1	141	2	S54236	Ig mu heavy chain

ALIGNMENTS

```
RESULT 1
S52446
Ig heavy chain V region precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 08-May-1995 #sequence_revision 03-Aug-1995 #text_change 23-Jul-1999
C/Accession: S52446
R/Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A/Description: Specific amplification by the polymerase chain reaction of rearranged gen
A/Reference number: S52445
A/Accession: S52446
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-141 <BER>
A/Cross-references: EMBL:X82692; NID:g673441; PID:CAA58013.1; PID:g673442
C/Genetics:
A/Intons: 16/1
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 588.5; DB 2; Length 141;
Best Local Similarity 81.0%; Pred. No. 9.5e-45;
Matches 115; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 MAVLVPLCLVAFPSCTL50VOLQESGPGIYKRSQTLSTCTVSGLSYGYWVROPP 60
    |||
Db 1 MAVLVPLCLVAFPSCTL50VOLQESGPGIYKRSQTLSTCTVSGLSYGYWVROPP 60
    |||

QY 61 GKLEWLVGVWAGTNNYSALMSRLTISKDNQVSLKSSVTADPAAVYCARGPPH 120
    |||
Db 61 GKLEWLVGVWAGTNNYSALMSRLTISKDNQVSLKSSVTADPAAVYCARGPPH 120
    |||

QY 121 AMMKRGYANDYWGQGLTVTVSS 142
    :
Db 120 STMDTPYANDYWGQGLTVTVSS 141
    :

RESULT 2
A32456
Ig heavy chain precursor V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C/Accession: A32456
R/Dombink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.
J. Biol. Chem. 264, 4513-4522, 1989
A/Title: Variable region primary structures of a high affinity anti-fluorescein immunogl
A/Reference number: A32456; M0ID:89174706; PMID:2494173
A/Accession: A32456
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-139 <DOM>
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A:Cross-references: GB:J04609; NID:9556316; PIDN:AAA50298.1; PID:9556317
 A:Note: the authors translated the codon CAC for residue 20 as Gln, and CAC for residue
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.7%; Score 561.5; DB 2; Length 139;
 Best Local Similarity 76.4%; Pred. No. 2.2e-42;
 Matches 110; Conservative 14; Mismatches 13; Indels 7; Gaps 2;

QY 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGGVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60
 DB 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGGVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60

QY 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAAADTAAYVYCAR 120
 DB 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAAADTAAYVYCAR 116

QY 121 AMMKR--GIAMDYWGQGTLLVTVSS 142
 DB 117 -RLERIFYVAMDYWGQGTSLTVSS 139

RESULT 3

SS5028
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
 C:Accession: S55028
 R:Jeffrey, P.D.; Schildbach, J.F.; Chang, C.Y.; Kussie, P.H.; Margolies, M.N.; Sheriff, J. Mol. Biol. 248, 344-360, 1995
 A:Title: Structure and specificity of the anti-digoxin antibody 40-50.
 A:Reference number: S55027; MUID:95257394; PMID:7739045
 A:Accession: S55028
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-140 <BSF>

A:Cross-references: EMBL:L11403; NID:9476717; PIDN:AAA38191.1; PID:9476718
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 75.2%; Score 558; DB 2; Length 140;
 Best Local Similarity 76.1%; Pred. No. 4.5e-42;
 Matches 108; Conservative 15; Mismatches 17; Indels 2; Gaps 1;

QY 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGGVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60
 DB 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGGVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60

QY 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAAADTAAYVYCAR 120
 DB 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAAADTAAYVYCAR 118

QY 121 AMMKRGVAMDYWGQGTLLVTVSS 142
 DB 119 PASYYDYAVDYWGQGTSLTVSS 140

RESULT 4

SS1913
 Ig gamma-2A chain precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 23-Jul-1999
 C:Accession: S31913
 R:Bespalov, I.A.; Hlyanov, P.A.; Lukashovich, L.V.; Lunev, V.B.; Tribush, S.S.; Gaponova
 submitted to the EMBL Data Library, January 1993
 A:Reference number: S31913
 A:Accession: S31913
 A:Molecule type: mRNA
 A:Residues: 1-135 <BRS>

A:Cross-references: EMBL:X70822; NID:957921; PIDN:CAA50153.1; PID:957922
 A:Experimental source: strain BALB/c

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-11/Domain: signal sequence #status predicted <SIG>
 F:12-135/Product: Ig gamma-2A chain (fragment) #status predicted <MAT>
 F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 71.2%; Score 528.5; DB 2; Length 135;
 Best Local Similarity 70.4%; Pred. No. 1.7e-39;
 Matches 100; Conservative 19; Mismatches 16; Indels 7; Gaps 1;

QY 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGGVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60
 DB 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGGVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60

QY 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAAADTAAYVYCAR 120
 DB 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAAADTAAYVYCAR 116

QY 121 AMMKRGVAMDYWGQGTLLVTVSS 142
 DB 117 --ELVYFDYWGQGTLLTVSS 135

RESULT 5

S10111
 Ig heavy chain V region (clone 26) precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S10111
 R:Kaartinen, M.; Solin, M.L.; Maekela, O.
 EMBO J. 8, 1743-1748, 1989
 A:Title: 'Allelic' forms of immunoglobulin V genes in different strains of mice.
 A:Reference number: S10111; MUID:89356648; PMID:2767052
 A:Accession: S10111
 A:Molecule type: mRNA
 A:Residues: 1-117 <KAA>

A:Cross-references: EMBL:X15471; NID:950005; PIDN:CAA33499.1; PID:950006
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 525; DB 2; Length 117;
 Best Local Similarity 85.3%; Pred. No. 2.9e-39;
 Matches 99; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGGVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60
 DB 1 MAVLVFLCLVAFPSCVLSQVQLQESGPGGVKPSQTLSTLTCTVSGFSLTSYGVWVRQPP 60

QY 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAAADTAAYVYCAR 116
 DB 61 GKGLEWLGIVMAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAAADTAAYVYCAR 116

RESULT 6

S14238
 Ig gamma-1 chain precursor (15C5) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S14238
 R:Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
 Eur. J. Biochem. 192, 767-775, 1990
 A:Title: Construction and characterization of a recombinant murine monoclonal antibody d.
 A:Reference number: S14236; MUID:91006173; PMID:2209622
 A:Accession: S14238
 A:Molecule type: mRNA
 A:Residues: 1-140 <VAN>

A:Cross-references: EMBL:X56392; NID:951619; PIDN:CAA39803.1; PID:9747853
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:26-108/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 510; DB 2; Length 140;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:49 ; Search time 6.62475 Seconds

(Without alignments)
1008.007 Million cell updates/sec

Title: US-09-772-103-10

Sequence: 1 MAVLVFLCLVAFPSCVLSQ.....MKRGVMDYMGCTLVTVSS 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	506	68.2	144	1	HV43_MOUSE
2	475	64.0	116	1	HV45_MOUSE
3	464	62.5	115	1	HV44_MOUSE
4	415	55.9	135	1	HV03_XENLA
5	414.5	55.9	146	1	HV21_HUMAN
6	390.5	52.6	137	1	HV46_MOUSE
7	379	51.1	117	1	HV26_HUMAN
8	376	50.7	129	1	HV2F_HUMAN
9	366	49.3	136	1	HV01_XENLA
10	361	48.7	116	1	HV61_MOUSE
11	352	47.4	116	1	HV60_MOUSE
12	342.5	46.2	147	1	HV2B_HUMAN
13	341.5	46.0	120	1	HV2B_HUMAN
14	339	45.7	121	1	HV3J_HUMAN
15	332.5	44.8	126	1	HV3K_HUMAN
16	332	44.7	113	1	HV44_MOUSE
17	329.5	44.4	122	1	HV3C_HUMAN
18	325	43.8	119	1	HV2C_HUMAN
19	324	43.7	125	1	HV2C_HUMAN
20	324	43.7	136	1	HV2C_RABIT
21	323.5	43.6	117	1	HV62_MOUSE
22	321.5	43.3	136	1	HV16_MOUSE
23	316.5	42.7	122	1	HV3H_HUMAN
24	310	41.8	121	1	HV2E_HUMAN
25	309	41.6	140	1	HV02_MOUSE
26	308.5	41.4	114	1	HV2A_RABIT
27	307.5	41.4	119	1	HV40_MOUSE
28	306	41.2	117	1	HV2B_RABIT
29	305	41.1	115	1	HV3D_HUMAN
30	304.5	41.0	142	1	HV01_RAT
31	304.5	41.0	119	1	HV3B_HUMAN
32	304.5	41.0	114	1	HV37_MOUSE
33	304.5	41.0	126	1	HV2A_HUMAN

34	304.5	41.0	137	1	HV11_MOUSE
35	302.5	40.8	139	1	HV07_MOUSE
36	302	40.7	116	1	HV05_CARAU
37	302	40.7	119	1	HV31_HUMAN
38	299	40.3	119	1	HV31_HUMAN
39	297	40.0	117	1	HV42_MOUSE
40	296	39.9	115	1	HV2F_HUMAN
41	295.5	39.8	116	1	HV3T_HUMAN
42	294	39.6	138	1	HV48_MOUSE
43	293.5	39.6	119	1	HV3P_HUMAN
44	292.5	39.4	116	1	HV1A_RABIT
45	292	39.4	120	1	HV03_MOUSE

ALIGNMENTS

RESULT 1

HV43_MOUSE STANDARD; PRT; 144 AA.

AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 141 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]

RP MEDLINE=81012133; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-681(1980)

CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

DR EMBL; V00768; CA24149.1; -
DR PIR; A02094; G2MS14.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 IG HEAVY CHAIN V REGION MOPC 141.
FT DOMAIN 20 IG-LIKE.
FT NON TER 144
SQ SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match Score 506; DB 1; Length 144;
Best Local Similarity 67.4%; Pred. No. 2e-42;
Matches 97; Conservative 15; Mismatches 30; Indels 2; Gaps 1;

QY 1 MAVLVFLCLVAFPSCVLSQGLVPSQTLSTCTVSGFSLTSYGVVWROPP 60
DB 1 MAVLVFLCLVAFPSCVLSQGLVPSQTLSTCTVSGFSLTSYGVVWROPP 60
QY 61 GKGLEWLGIVAGGTTNYSALMSRLTISKDSKNQVSLKSTVTAADTAVYYCARGP-- 118

Db 61 GKGLEMLGVTWNGSGSTYNSLTSLKRLITTKDNKNSQVFLKNNLSQTDPTARYCAVSIV 120
 QY 119 PHAMKRGYADYWGQGLTVTVSS 142
 Db 121 YGGRSDKFTLDTWGGQSTVTVSS 144

RESULT 2

HV45_MOUSE
 ID HV45_MOUSE STANDARD; PRT; 116 AA.

AC P01821;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region MC101 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

EMBL: J00502; AAA38515.1; -

PIR: A02096; G1MS10.

HSSP: P01772; 2FB4.

InterPro: IPR007110; IG-like.

InterPro: IPR003006; IG_MHC.

InterPro: IPR003596; IG_V.

Pfam: PF00047; IG_1.

SMART: SM00406; IG_V.

SMART: SM00406; IG_V.

PROSITE: PS50835; IG-LIKE.

PROSITE: PS50835; IG-LIKE.

IMMUNOGLOBULIN V region; Signal.

FT CHAIN 1 19 IG HEAVY CHAIN V REGION MC101.

FT DOMAIN 20 116 IG-LIKE.

FT NON_TER 116 116

FT NON_TER 116 116

SEQUENCE 116 AA; 12593 MW; 8079A6EB7C552B3E CRC64;

Query Match

Best Local Similarity 64.0%; Score 475; DB 1; Length 116;

Matches 87; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

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Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

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QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

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QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

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Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

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QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

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QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

QY 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

Db 1 MAVLVFLCLVAFPSCTLSQVLOESGPGVLKPSQTLSTCTVSGFSLTSYGVMWRPP 60

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region P014 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;

RESULT 4

HV02_XENIA
 ID HV02_XENIA STANDARD; PRT; 135 AA.

AC P20957;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V region XIG14 precursor (Fragment).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OC Xenopodinae; Xenopus.

CC or send an email to license@lsb-sib.ch).

EMBL: V00767; CA24148.1; -

PIR: A02095; HVMS14.

PDB: 1A7N; 29-APR-98.

PDB: 1A7O; 29-APR-98.

PDB: 1A7P; 29-APR-98.

PDB: 1A7R; 29-APR-98.

PDB: 1G7H; 17-JAN-01.

PDB: 1G7I; 17-JAN-01.

PDB: 1G7J; 17-JAN-01.

PDB: 1G7K; 17-JAN-01.

PDB: 1G7L; 17-JAN-01.

PDB: 1G7M; 17-JAN-01.

PDB: 1G7N; 17-JAN-01.

PDB: 1G7O; 17-JAN-01.

PDB: 1G7P; 17-JAN-01.

PDB: 1G7Q; 17-JAN-01.

PDB: 1G7R; 17-JAN-01.

PDB: 1G7S; 17-JAN-01.

PDB: 1G7T; 17-JAN-01.

PDB: 1G7U; 17-JAN-01.

PDB: 1G7V; 17-JAN-01.

PDB: 1G7W; 17-JAN-01.

PDB: 1G7X; 17-JAN-01.

PDB: 1G7Y; 17-JAN-01.

PDB: 1G7Z; 17-JAN-01.

PDB: 1G8A; 17-JAN-01.

PDB: 1G8B; 17-JAN-01.

PDB: 1G8C; 17-JAN-01.

PDB: 1G8D; 17-JAN-01.

PDB: 1G8E; 17-JAN-01.

PDB: 1G8F; 17-JAN-01.

PDB: 1G8G; 17-JAN-01.

PDB: 1G8H; 17-JAN-01.

PDB: 1G8I; 17-JAN-01.

PDB: 1G8J; 17-JAN-01.

PDB: 1G8K; 17-JAN-01.

PDB: 1G8L; 17-JAN-01.

PDB: 1G8M; 17-JAN-01.

PDB: 1G8N; 17-JAN-01.

PDB: 1G8O; 17-JAN-01.

PDB: 1G8P; 17-JAN-01.

PDB: 1G8Q; 17-JAN-01.

PDB: 1G8R; 17-JAN-01.

PDB: 1G8S; 17-JAN-01.

PDB: 1G8T; 17-JAN-01.

PDB: 1G8U; 17-JAN-01.

PDB: 1G8V; 17-JAN-01.

PDB: 1G8W; 17-JAN-01.

PDB: 1G8X; 17-JAN-01.

PDB: 1G8Y; 17-JAN-01.

PDB: 1G8Z; 17-JAN-01.

PDB: 1G9A; 17-JAN-01.

PDB: 1G9B; 17-JAN-01.

PDB: 1G9C; 17-JAN-01.

PDB: 1G9D; 17-JAN-01.

PDB: 1G9E; 17-JAN-01.

PDB: 1G9F; 17-JAN-01.

PDB: 1G9G; 17-JAN-01.

PDB: 1G9H; 17-JAN-01.

PDB: 1G9I; 17-JAN-01.

PDB: 1G9J; 17-JAN-01.

PDB: 1G9K; 17-JAN-01.

PDB: 1G9L; 17-JAN-01.

PDB: 1G9M; 17-JAN-01.

PDB: 1G9N; 17-JAN-01.

PDB: 1G9O; 17-JAN-01.

PDB: 1G9P; 17-JAN-01.

PDB: 1G9Q; 17-JAN-01.

PDB: 1G9R; 17-JAN-01.

PDB: 1G9S; 17-JAN-01.

PDB: 1G9T;

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:33:29 ; Search time 24.1947 Seconds
(without alignments)
1514.523 Million cell updates/sec

Title: US-09-772-103-10
 Perfect score: 742
 Sequence: 1 MAVLVFLCLVAFPSCVLSQ.....MKRGYAMDYMGQGLVTYSS 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```

1:  sp_archaea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:  sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioid:*
17: sp_archaeop:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	526.5	71.0	482	11	Q91X92	Q91X92 mus musculi
	2	467.5	63.0	613	4	Q96EY0	Q96EY0 homo sapien
	3	462.5	60.3	121	11	Q9NKG4	Q9NKG4 mus musculi
	4	449.5	60.6	496	4	Q96KX8	Q96KX8 homo sapien
	5	437	58.7	119	4	Q9UL73	Q9UL73 homo sapien
	6	435.5	58.9	150	4	Q9SE973	Q9SE973 homo sapien
	7	429	57.8	588	4	Q8WUX4	Q8WUX4 homo sapien
	8	429	57.8	597	4	Q9BU10	Q9BU10 homo sapien
	9	429	57.8	618	4	Q96AA6	Q96AA6 homo sapien
	10	437	57.5	497	4	Q9BQB8	Q9BQB8 homo sapien
	11	397.5	53.6	473	4	Q8RFC3	Q8RFC3 homo sapien
	12	392.5	52.9	479	11	Q9NMZ2	Q9NMZ2 mus musculi
	13	383.5	51.7	130	4	O81ZD7	O81ZD7 homo sapien
	14	374	50.4	121	4	Q9UL96	Q9UL96 homo sapien
	15	351	47.3	597	4	Q9EBH9	Q9EBH9 homo sapien
	16	346.5	46.7	122	4	Q9UL75	Q9UL75 homo sapien

17	344.5	46.4	112	4	Q9HCCL	Q9hcc1 homo sapien
18	340	45.8	493	4	Q8NC6	Q8nc6 homo sapien
19	338.5	45.6	573	4	Q8WU38	Q8wu38 homo sapien
20	337	44.5	499	4	Q8NSK4	Q8nsk4 homo sapien
21	330.5	44.5	613	4	Q8WUK1	Q8wuk1 homo sapien
22	326	43.5	116	4	Q9UL93	Q9ul93 homo sapien
23	325	43.8	481	11	Q91WT1	Q91wt1 mus musculus
24	323	43.5	113	4	Q9UL90	Q9ul90 homo sapien
25	323	43.5	131	4	Q9UL88	Q9ul88 homo sapien
26	322	43.4	142	11	Q924Q1	Q924q1 mus musculus
27	321	43.3	121	4	Q9UL71	Q9ul71 homo sapien
28	319.5	43.1	124	4	Q9UL92	Q9ul92 homo sapien
29	318.5	42.9	147	4	Q9Y509	Q9y509 homo sapien
30	318.5	42.9	488	11	Q91WR1	Q91wr1 mus musculus
31	318.5	42.9	613	11	Q8VCX7	Q8vcx7 mus musculus
32	317.5	42.8	122	4	Q9UL84	Q9ul84 homo sapien
33	317.5	42.8	487	11	Q99KA4	Q99ka4 mus musculus
34	316.5	42.7	469	11	Q8R3V9	Q8r3v9 mus musculus
35	316.5	42.7	473	11	Q91Z05	Q91z05 mus musculus
36	315.5	42.5	145	11	Q924Q6	Q924q6 mus musculus
37	315.5	42.5	145	11	Q924Q9	Q924q9 mus musculus
38	315	42.5	119	11	Q920E7	Q920e7 mus musculus
39	313.5	42.3	118	4	Q9UL72	Q9ul72 homo sapien
40	312.5	42.1	143	11	Q924R0	Q924r0 mus musculus
41	311.5	42.0	124	6	Q9N0M6	Q9n0m6 Oryctolagus
42	311.5	42.0	482	11	Q8K172	Q8k172 mus musculus
43	311	41.9	146	11	Q924Q3	Q924q3 mus musculus
44	310.5	41.8	145	11	Q924P7	Q924p7 mus musculus
45	310.5	41.8	145	11	Q924R1	Q924r1 mus musculus

RESULT 1	ID	PRELIMINARY;	PRT;	482 AA.
091X92	AC	091X92;		
DT	01-DEC-2001	(TREMBLERel. 19, Created)		
DT	01-DEC-2001	(TREMBLERel. 19, Last sequence update)		
DT	01-MAR-2003	(TREMBLERel. 23, Last annotation update)		
DE	Unknown	(Protein for MGC:18822)		
OS	Mus musculus	(Mouse)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	NCBI_TaxID=10090;			
RP	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Colon;			
RA	Strausberg R.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC011181; AAH1181.1; -			
DR	InterPro; IPR007110; IG_1ike			
DR	InterPro; IPR003006; IG_MHC			
DR	InterPro; IPR003596; IG_v			
DR	Pfam; PF00047; Ig_4			
DR	SMART; SM00406; IgV_1			
DR	PROSITE; PSS0835; IG_LIKE; 4			
DR	PROSITE; PSS00290; IG_MHC; 2			
SO	SEQUENCE 482 AA; 51865 MW; 312E01F9C1BC73C CRC64;			
Query Match 71.0%; Score 526.5; DB 11; Length 482;				
Best Local Similarity 72.5%; Pred. No. 2.9e-47;				
Matches 103; Conservative 11; Mismatches 23; Indels 5; Gaps 1				
QY	1	MAVLVFLCLVAPPSCVLSQVQLQESPPGAVKPSQTLSTLTCTGVSFSLTSYGVYVWRQP	60	
Db	1	MAVLALLLCLVTPPSCALSVQLKESPPDLVARSQSLITCTYSGFALTSIAISWRQP	60	
QY	61	GKGLKMLGVIMAGTGNYNALSRLTISKDTSKNQVSLKSSVTADTAAYVYCARGPBH	120	
Db	61	GKGLKMLGVIMAGTGNYNALSRLTISKDTSKNQVSLKSSVTADTAAYVYCARGSNY	120	

QY 121 AMMKRGYAMDYGGLTVYSS 142
 DB 121 E-----GAMDYGGGTSVTYSS 137

RESULT 2

Q96EYO PRELIMINARY; PRT; 613 AA.

AC Q96EYO; 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=B-cell;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC011857; AAH11857.1; -

DR InterPro: IPR007110; I9_1like.

DR InterPro: IPR003006; I9_MHC.

DR Pfam: PF00047; I9_5.

DR SMART: SM00406; IGV_1.

DR PROSITE: PS50835; IG_LIKE; 5.

DR PROSITE: PS00290; IG_MHC; 3.

KW Hypothetical protein.

SEQUENCE 613 AA; 67273 MW; 31214203FB8421E7 CRC64;

Query Match 63.0%; Score 467.5; DB 4; Length 613;

Best Local Similarity 68.3%; Pred. No. 6.9e-41;

Matches 99; Conservative 11; Mismatches 26; Indels 9; Gaps 2;

QY 1 MAVLVFLCLVAFPSCVLSQVLOESGPGLVKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60

DB 1 MKHLWFLFLVAPRWVLSQVLOESGPGLVKPSQTLSTCTVSGFSLTSYGVYVWRQPP 60

QY 61 GKGLWLVIMAGTNNYNSALMSRLTISKDTSKNOVSLKLSVTAADTAAYVCARGP-- 118

DB 61 GKGLWLVIMAGTNNYNSALMSRLTISKDTSKNOVSLKLSVTAADTAAYVCARGP-- 120

QY 119 -PHAMMKRGYAMDYGGLTVYSS 142

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

QY 121 LPTV-----GLFTYGGGTLVYSS 139

DB 121 LPTV-----GLFTYGGGTLVYSS 139

DR InterPro: IPR007110; I9_1like.
 DR InterPro: IPR003006; I9_MHC.
 DR InterPro: IPR003596; I9_V.
 DR Pfam: PF00047; I9_1.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Plasmid.
 FT NON TER 121 121
 SQ SEQUENCE 121 AA; 13255 MW; D2934EBC6C59D5B CRC64;

Query Match 62.3%; Score 462.5; DB 11; Length 121;

Best Local Similarity 73.2%; Pred. No. 3e-41;

Matches 90; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

QY 20 QVLOESGPGLVKPSQTLSTCTVSGFSLTSYGVYVWRQPPKGLWLVIMAGTNNYN 79

DB 1 QVLOESGPGLVKPSQTLSTCTVSGFSLTSYGVYVWRQPPKGLWLVIMAGTNNYN 60

QY 80 SALMSRLTISKDTSKNOVSLKLSVTAADTAAYVCARGP--PHAMMKRGYAMDYGGLTVT 139

DB 61 SALMSRLTISKDTSKNOVSLKLSVTAADTAAYVCARGP--PHAMMKRGYAMDYGGLTVT 117

QY 140 VSS 142

DB 118 VSS 120

QY 140 VSS 142

DB 118 VSS 120

QY 140 VSS 142

DB 118 VSS 120

QY 140 VSS 142

DB 118 VSS 120

QY 140 VSS 142

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QY 140 VSS 142

DB 118 VSS 120

QY 140 VSS 142

DB 118 VSS 120

QY 140 VSS 142

DB 118 VSS 120

QY 140 VSS 142

DB 118 VSS 120

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:32:09 | Search time 30.2434 Seconds
(without alignments)
745.259 Million cell updates/sec

Title: US-09-772-103-10
742
1 MAVLVLPLCLVAFPSCVLSQ.....MKRGYANDYWGQGLTVTVSS 142
Perfect score:

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: A_Geneseq_19Jun03:*
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23: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
24: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
25: /SIDSI1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	742	100.0	142	22	AA66523 Humanised anti-CTL
2	664	89.5	142	22	AA66520 Mouse antibody 26
3	632	85.2	140	23	ABP51940 Silenced anti-CD28
4	603.5	81.3	137	18	AAW30273 Heavy chain of Hum
5	545	73.5	140	18	AAW22538 Murine anti-human
6	545	73.5	140	23	AAE20201 Murine 44H104 mab
7	542	73.0	478	23	ABG31730 Murine m166 antibo
8	541.5	73.0	137	22	AAH81975 Ganglioside GD2 sp
9	530	71.4	151	17	AAH98941 Humanised anti-CD3

10	529.5	71.4	135	8	AAH70991	Sequence of the he
11	527.5	71.1	137	18	AAW30277	Heavy chain of MuM
12	527	71.0	138	17	AAW01146	Mab 10.1 heavy cha
13	525	70.8	119	17	AAH98492	NEWM humanised 2B6
14	525	70.8	138	22	AAH69656	Murine m166 antibo
15	522	70.4	119	19	AAW42471	NEWM humanised hea
16	518	69.8	138	18	AAW08942	Heavy chain variab
17	515.5	69.5	116	17	AAW05823	Humanised ID10 ant
18	515.5	69.5	273	17	AAW05827	Humanised ID10 ant
19	515.5	69.5	446	17	AAW05829	Humanised ID10 ant
20	515	69.4	138	18	AAW08944	Heavy chain variab
21	515	69.4	183	12	AAH15326	IL-2 chimeric anti
22	515	69.4	183	14	AAH32128	Anti-IL2R-alpha an
23	514	69.3	152	20	AAH49210	Mab 1A7 heavy chai
24	514	69.3	152	20	AAH28469	Heavy chain variab
25	514	69.3	152	20	AAH21546	Monoclonal antibod
26	514	69.3	263	20	AAH28470	Vh-(Lk)-Vl of anti
27	512.5	69.1	139	23	AAH79726	Anti-Streptococcus
28	509	68.6	152	17	AAW03200	Anti-Idiotypic mono
29	508	68.5	358	23	AAE27929	Human CH2 domain d
30	508	68.5	358	24	AAE82838	Antibody C5E10 CH2
31	508	68.5	468	23	AAE27928	Human C5E10 antibo
32	508	68.5	468	24	AAH82837	Antibody C5E10 hea
33	507.5	68.4	120	20	AAH22432	TM27 antibody VH c
34	507	68.3	144	17	AAH98944	Humanised anti-CD3
35	504.5	68.0	118	22	AAH81970	Ganglioside GD2 sp
36	504.5	68.0	120	20	AAH22429	TM27 antibody VH c
37	504.5	68.0	581	22	AAH81972	TM27 antibody VH c
38	503.5	67.9	120	20	AAH22431	Ganglioside GD2 sp
39	502.5	67.7	120	20	AAH22430	TM27 antibody VH c
40	498.5	67.2	133	18	AAH10546	Wild type murine a
41	497.5	67.0	120	20	AAH22433	TM27 antibody VH c
42	494.5	66.6	120	16	AAH77303	Variable heavy cha
43	494.5	66.6	193	23	AAH43199	Human ovarian anti
44	493.5	66.5	120	24	AAH16027	Cyclic single-stra
45	492.5	66.4	132	15	AAH53331	KM-603 heavy chain

ALIGNMENTS

RESULT 1	AA66523	standard; Protein; 142 AA.
ID	AA66523;	
AC	AA66523;	
XX		
DT	22-OCT-2001 (first entry)	
XX		
DE	Humanised anti-CTLA4 heavy chain.	
KW	Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;	
KW	immunopressive; immunomodulator; antiallergic; vaccine; antibody;	
KW	T cell; humanised antibody; autoimmune disorder; graft rejection;	
KW	allergy; heavy chain.	
OS	Homo sapiens.	
OS	Mus musculus.	
OS	Synthetic.	
PN	WO200154732-A1.	
XX		
PD	02-AUG-2001.	
XX		
PF	26-JAN-2001; 2001WO-US02653.	
XX		
PR	27-JAN-2000; 2000US-0178473.	
XX		
PA	(GENEY) GENETICS INST INC.	
XX		
PI	Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;	
PI	O'Hara D, Hinton P, Teurshilta N;	
XX		

DR WPI: 2001-483195/52.
 DR N-PSDB; AAH76441, AAH76443.
 XX Novel antibody-toxic group conjugate comprising an antibody that
 PT recognizes a molecule expressed only on activated T cells, useful for
 PT modulating immune response for treating autoimmune disorder, allergic
 PT response
 XX Claim 15; Fig 10; 123pp; English.

CC The invention relates to an antibody-toxic group conjugate comprising
 CC an antibody that specifically recognises a molecule expressed only on
 CC activated T cells, and a toxic group. The T cell molecule is
 CC preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).
 CC The antibody of the invention is a humanised anti-CTLA4 antibody
 CC comprising a sequence of 128 or 142 amino acids fully defined in the
 CC specification. The antibody-toxic group conjugate is useful for
 CC modulating the immune response in a subject suffering from a disorder
 CC or condition such as autoimmune disorder, immune response to a graft,
 CC allergic response or an immune response to a therapeutic protein.
 CC The antibody is also useful for research purposes, e.g., in staining
 CC and isolating CTLA4-bearing cells. The antibody is also useful for
 CC T-cell typing, for isolating specific IL-2 receptor-bearing cells or
 CC fragments of the receptor, for vaccine preparation, and for determining
 CC the effectiveness of an agent to down-regulate CTLA4 activity. The
 CC present sequence is the heavy chain of humanised anti-CTLA4
 CC antibody.

XX Sequence 142 AA:

Query Match 100.0%; Score 742; DB 22; Length 142;
 Best Local Similarity 100.0%; Pred. No. 8.1e-60;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVVLVFLCLVAPSCVLSQVLOESGPGVLPKPSQTLSTCTVSGFSLTGYWYRPP 60
 DB 1 MAVVLVFLCLVAPSCVLSQVLOESGPGVLPKPSQTLSTCTVSGFSLTGYWYRPP 60
 QY 61 GKLEMLGVIMAGGTNNYSALMSRLTISKDTSKNQVSLKSTVADTAVYCARPPH 120
 DB 61 GKLEMLGVIMAGGTNNYSALMSRLTISKDTSKNQVSLKSTVADTAVYCARPPH 120
 QY 121 AMMKRGYAMDYWGQGLTVTVSS 142
 DB 121 AMMKRGYAMDYWGQGLTVTVSS 142

RESULT 2
 AAG66520
 ID AAG66520 standard; Protein; 142 AA.

XX AAG66520;
 XX 22-OCT-2001 (first entry)

DE Mouse antibody 26 heavy chain variable region.

XX Mouse; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
 KM immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
 KM T cell; humanised antibody; autoimmune disorder; graft rejection;
 KM allergy; antibody 26; heavy chain variable region; VH.

XX Mus musculus.

XX WO200154732-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US02653.

XX 27-JAN-2000; 2000US-0178473.

XX (GENY) GENETICS INST INC.

XX Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
 PI O'Hara D, Hinton P, Tsurushita N;
 XX WPI: 2001-483195/52.
 DR N-PSDB; AAH76438.

XX Novel antibody-toxic group conjugate comprising an antibody that
 PT recognizes a molecule expressed only on activated T cells, useful for
 PT modulating immune response for treating autoimmune disorder, allergic
 PT response

XX Example 7; Page 84; 123pp; English.

CC The invention relates to an antibody-toxic group conjugate comprising
 CC an antibody that specifically recognises a molecule expressed only on
 CC activated T cells, and a toxic group. The T cell molecule is
 CC preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).
 CC The antibody of the invention is a humanised anti-CTLA4 antibody
 CC comprising a sequence of 128 or 142 amino acids fully defined in the
 CC specification. The antibody-toxic group conjugate is useful for
 CC modulating the immune response in a subject suffering from a disorder
 CC or condition such as autoimmune disorder, immune response to a graft,
 CC allergic response or an immune response to a therapeutic protein.
 CC The antibody is also useful for research purposes, e.g., in staining
 CC and isolating CTLA4-bearing cells. The antibody is also useful for
 CC T-cell typing, for isolating specific IL-2 receptor-bearing cells or
 CC fragments of the receptor, for vaccine preparation, and for determining
 CC the effectiveness of an agent to down-regulate CTLA4 activity. The
 CC present sequence is the heavy chain variable region of mouse
 CC antibody 26. It was used in the construction of the humanised anti-CTLA4
 CC antibody of the invention.

XX Sequence 142 AA:

Query Match 89.5%; Score 664; DB 22; Length 142;
 Best Local Similarity 88.0%; Pred. No. 9.8e-53;
 Matches 125; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAVVLVFLCLVAPSCVLSQVLOESGPGVLPKPSQTLSTCTVSGFSLTGYWYRPP 60
 DB 1 MDVLVFLCLVAPSCVLSQVLOESGPGVLPKPSQTLSTCTVSGFSLTGYWYRPP 60
 QY 61 GKLEMLGVIMAGGTNNYSALMSRLTISKDTSKNQVSLKSTVADTAVYCARPPH 120
 DB 61 GKLEMLGVIMAGGTNNYSALMSRLTISKDTSKNQVSLKSTVADTAVYCARPPH 120
 QY 121 AMMKRGYAMDYWGQGLTVTVSS 142
 DB 121 AMMKRGYAMDYWGQGLTVTVSS 142

RESULT 3
 ABP51940
 ID ABP51940 standard; Protein; 140 AA.

XX ABP51940;

XX 08-OCT-2002 (first entry)

DE Silenced anti-CD28 antibody heavy chain protein SEQ ID NO:6.

XX Silenced anti-CD28 antibody; mitogenic; immunosuppressive; antirheumatic;
 KM antiarthritic; antiinflammatory; dermatological; neuroprotective; asthma;
 KM antidiabetic; antiallergic; T-cell tolerance inducer; myasthenia gravis;
 KM tissue transplant rejection; graft-versus host disease; type I diabetes;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM multiple sclerosis; immune disease; immune reaction suppressor;
 KM atopic dermatitis.

XX Homo sapiens.

XX Synthetic.

Tue Dec 2 07:00:55 2003

us-09-772-103-10.rapb

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:44:30 ; Search time 20.4503 Seconds
(without alignments) 1280.712 Million cell updates/sec

Title: US-09-772-103-10

Perfect score: 742
Sequence: 1 MAVVLFLCLVAFPSCVLSQ.....MKRGVANDYMGQTLVTVSS 142

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	545	72.5	140	9	US-09-007-093-4
2	539.5	72.7	139	8	US-08-779-784-37
3	530	71.4	151	10	US-09-797-941A-2
4	527.5	71.1	135	8	US-08-779-784-32
5	525	70.8	119	15	US-10-144-644-62
6	522.5	70.4	135	12	US-10-010-729-68
7	514	69.3	152	10	US-09-990-205-4
8	514	69.3	152	15	US-10-153-401-4
9	514	69.3	263	15	US-10-153-401-66
10	512.5	69.1	139	9	US-09-881-823-4
11	511.5	68.9	141	15	US-10-207-655-359
12	507	68.3	144	10	US-09-797-941A-8
13	494.5	66.6	250	15	US-10-194-975-110
14	485	65.4	119	15	US-10-144-644-15
15	478	64.4	121	15	US-10-056-052-20

16	472	63.6	119	15	US-10-144-644-19	Sequence 19, Appl
17	471	63.5	119	15	US-10-153-401-16	Sequence 16, Appl
18	468	63.1	333	15	US-10-059-261-61	Sequence 61, Appl
19	466.5	62.9	120	15	US-10-194-975-112	Sequence 112, App
20	466	62.8	119	14	US-10-025-687-5	Sequence 5, Appl
21	466	62.8	119	15	US-10-125-687-5	Sequence 5, Appl
22	466	62.8	249	9	US-09-730-374-3	Sequence 3, Appl
23	463	62.4	119	15	US-10-232-187-2	Sequence 2, Appl
24	462.5	62.3	121	12	US-10-010-729-11	Sequence 11, Appl
25	461.5	62.2	116	15	US-10-169-351-108	Sequence 108, App
26	458.5	61.8	116	15	US-10-194-975-100	Sequence 100, App
27	458.5	61.8	1487	9	US-09-800-729-145	Sequence 145, App
28	456	61.5	116	9	US-09-881-823-18	Sequence 18, Appl
29	453.5	61.1	112	9	US-09-824-286-3	Sequence 3, Appl
30	451	60.8	271	15	US-10-207-655-254	Sequence 254, App
31	451	60.8	556	15	US-10-207-655-268	Sequence 268, App
32	447.5	60.3	139	12	US-10-300-675-2	Sequence 2, Appl
33	447	60.2	121	15	US-10-207-655-252	Sequence 252, App
34	446.5	60.2	119	14	US-10-140-555-2	Sequence 2, Appl
35	444.5	59.9	126	15	US-10-067-800-68	Sequence 68, Appl
36	443	59.7	117	12	US-10-330-613-13	Sequence 13, Appl
37	443	59.7	117	12	US-10-330-530-13	Sequence 362, App
38	442.5	59.6	271	15	US-10-207-655-362	Sequence 363, App
39	442.5	59.6	505	15	US-10-207-655-363	Sequence 364, App
40	442.5	59.6	536	15	US-10-207-655-364	Sequence 35, Appl
41	442	59.6	580	12	US-10-310-719-37	Sequence 37, Appl
42	442	59.6	580	12	US-10-310-719-37	Sequence 360, App
43	438.5	59.1	122	15	US-10-207-655-360	Sequence 990, App
44	438	59.0	251	11	US-09-880-748-990	Sequence 1329, App
45	437.5	59.0	252	11	US-09-880-748-1329	

ALIGNMENTS

RESULT 1
US-09-007-093-4
Sequence 4, Application US/09007093
Patent No. US20020025315A1
GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Caterini, George A
APPLICANT: Caterini, Judith E
APPLICANT: Klein, Michel H
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,093
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-765
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-007-093-4

Query Match 73.5%; Score 545; DB 9; Length 140;
Best Local Similarity 76.2%; Pred. No. 1,1e-44;
Matches 109; Conservative 12; Mismatches 18; Indels 4; Gaps 2;

QY 1 MAVLVFLCLVAFPSGCVLSQVQLQESGPGGLVYPKSQTLSLTCTVSGFSLTSYGVYWRQP 59
DB 1 MAVLVFLCLVAFPSGCVLSQVQLQESGPGGLVYPKSQTLSLTCTVSGFSLTSYGVYWRQP 60
QY 60 PGKLEWLVGIYVAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAAYVCARGPP 119
DB 61 PGKLEWLVGIYVAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAAYVCARGPP 120
QY 120 HAMMKRGVANDYWGCGTLTVYSS 142
DB 121 DYV---HYAMDYWGCGTSTVYSS 140

RESULT 2

US-08-779-784-37
Sequence 37, Application US/08779784
Publication No. US20020164325A1
GENERAL INFORMATION:

APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
NUMBER OF SEQUENCES: 37
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-772-103-10.rapb

MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-779-784-37

Query Match 72.7%; Score 539.5; DB 8; Length 139;
Best Local Similarity 71.2%; Pred. No. 3.8e-44;
Matches 104; Conservative 17; Mismatches 14; Indels 11; Gaps 2;

QY 1 MAVLVFLCLVAFPSGCVLSQVQLQESGPGGLVYPKSQTLSLTCTVSGFSLTSYGVYWRQP 60
DB 1 MAVLVFLCLVAFPSGCVLSQVQLQESGPGGLVYPKSQTLSLTCTVSGFSLTSYGVYWRQP 60
QY 61 GKLEWLVGIYVAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAAYVCARGPP 120
DB 61 GKLEWLVGIYVAGGTTNYSALMSRLTISKDTSKNOVSLKSSVTAADTAAYVCARGPP 116
QY 121 AMMKRG---YAMDYWGCGTLTVYSS 142
DB 117 ---NRGRVYVAMDYWGCGTSTVYSS 139

RESULT 3

US-09-797-941A-2
Sequence 2, Application US/09797941A
Patent No. US20020164788A1
GENERAL INFORMATION:

APPLICANT: ELLIS, JONATHAN H.
LEWIS, ALAN P.
TITLE OF INVENTION: HUMANISED ANTIBODIES TO CD18
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSER: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/797,941A
FILING DATE: 05-Mar-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/849,410
FILING DATE: 30-MAY-1997
APPLICATION NUMBER: PCT/GB95/02777
FILING DATE: 28-NOV-1995
APPLICATION NUMBER: GB 9424449.8
FILING DATE: 02-DEC-1994
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-797-941A-2

Query Match 71.4%; Score 530; DB 10; Length 151;
Best Local Similarity 69.7%; Pred. No. 3.4e-43;
Matches 99; Conservative 19; Mismatches 20; Indels 4; Gaps 1;

QY 1 MAVLVFLCLVAFPSGCVLSQVQLQESGPGGLVYPKSQTLSLTCTVSGFSLTSYGVYWRQP 60
DB 3 LAVLVFLCLVAFPSGCVLSQVQLQESGPGGLVYPKSQTLSLTCTVSGFSLTSYGVYWRQP 62

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OM protein - protein search, using sw model

Run on: December 2, 2003, 06:40:15; Search time 10.9452 Seconds

(without alignments)
548.928 Million cell updates/sec

Title: US-09-772-103-10

Perfect score: 742

Sequence: 1 MAVLVFLGLVAFPSCVLSQ.....MKGYANDYWGQGLVTYVSS 142

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 4231088 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*

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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the chance being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 603.5 81.3 137 2 US-08-621-751A-8 Sequence 8, Appl1

2 545 73.5 140 3 US-08-943-136-4 Sequence 4, Appl1

3 545 73.5 140 4 US-08-973-518-4 Sequence 4, Appl1

4 527.5 70.8 137 2 US-08-621-751A-4 Sequence 4, Appl1

5 525 70.8 119 1 US-08-667-769A-2 Sequence 62, Appl1

6 525 70.8 119 5 PCT-US95-17082A-62 Sequence 33, Appl1

7 525 70.8 138 1 US-07-634-278-33 Sequence 33, Appl1

8 525 70.8 138 1 US-08-474-728-33 Sequence 33, Appl1

9 525 70.8 138 1 US-08-474-040-33 Sequence 33, Appl1

10 525 70.8 138 1 US-08-467-200-33 Sequence 33, Appl1

11 525 70.8 138 3 US-08-484-537-33 Sequence 33, Appl1

12 521 70.2 119 1 US-08-467-420A-62 Sequence 62, Appl1

13 521 70.2 119 1 US-08-940-110A-62 Sequence 62, Appl1

14 521 70.2 119 2 US-08-940-371-62 Sequence 62, Appl1

15 515.5 69.5 272 3 US-08-397-411-3 Sequence 3, Appl1

16 515.5 69.5 272 3 US-08-397-411-6 Sequence 6, Appl1

17 515.5 69.5 446 3 US-08-397-411-7 Sequence 7, Appl1

18 514 69.3 152 2 US-08-752-844-4 Sequence 4, Appl1

19 514 69.3 152 2 US-08-591-196-4 Sequence 4, Appl1

20 514 69.3 152 4 US-09-192-838B-4 Sequence 4, Appl1

21 514 69.3 152 4 US-09-293-533-4 Sequence 4, Appl1

22 514 69.3 152 4 US-09-324-191-4 Sequence 4, Appl1

23 514 69.3 263 2 US-08-752-844-66 Sequence 66, Appl1

24 514 69.3 263 4 US-09-293-533-66 Sequence 66, Appl1

25 507.5 68.4 120 2 US-08-652-558-8 Sequence 8, Appl1

26 507.5 68.4 120 3 US-09-254-189-5 Sequence 5, Appl1

27 504.5 68.0 120 2 US-08-652-558-4 Sequence 4, Appl1

28 504.5 68.0 120 2 US-08-652-558-5 Sequence 5, Appl1

29 504.5 68.0 120 3 US-09-254-189-2 Sequence 2, Appl1

30 503.5 67.9 120 2 US-08-652-558-7 Sequence 7, Appl1

31 503.5 67.9 120 3 US-09-254-189-4 Sequence 4, Appl1

32 502.5 67.7 120 2 US-08-652-558-6 Sequence 6, Appl1

33 502.5 67.7 120 3 US-09-254-189-3 Sequence 3, Appl1

34 497.5 67.0 120 2 US-08-652-558-9 Sequence 9, Appl1

35 497.5 67.0 120 3 US-09-254-189-6 Sequence 6, Appl1

36 485.5 65.4 120 4 US-08-057-430A-26 Sequence 26, Appl1

37 485 65.4 119 1 US-08-667-769A-15 Sequence 15, Appl1

38 485 65.4 119 5 PCT-US95-17082A-15 Sequence 15, Appl1

39 482.5 65.0 120 2 US-08-353-372A-36 Sequence 36, Appl1

40 482 65.0 142 2 US-08-480-774A-2 Sequence 2, Appl1

41 481.5 64.9 473 3 US-09-049-672A-4 Sequence 4, Appl1

42 479.5 64.6 121 3 US-08-881-037-67 Sequence 67, Appl1

43 476 64.2 222 2 US-08-190-199A-67 Sequence 67, Appl1

44 476 64.2 235 2 US-08-190-199A-61 Sequence 61, Appl1

45 472.5 63.7 242 6 5455030-15 Patent No. 5455030

ALIGNMENTS

RESULT 1

US-08-621-751A-8

Sequence 8, Application US/08621751A

Patent No. 5882644

GENERAL INFORMATION:

APPLICANT: Chang, Chung N.

APPLICANT: Landolfi, Nicholas F.

TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE

TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTOR BETA RECEPTOR AND

TITLE OF INVENTION: METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSER: MORRISON & FOERSTER LLP

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,751A

FILING DATE: 22-MAR-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: leinhardt, Susan K.

REGISTRATION NUMBER: 33,943

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141 MRSN FOERS SFO

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 137 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

US-08-621-751A-8

Query Match 81.3%, Score 603.5, DB 2, Length 137;

Best local similarity 83.1%; Pred. No. 1e-54;

Matches 118; Conservative 5; Mismatches 14; Indels 5; Gaps 1;

1 MAVLVFLGLVAFPSCVLSQ.....MKGYANDYWGQGLVTYVSS 142

Db 1 MAVLALUCLVTFPSICALSQVLOESGPGLVKPSSETLSLTCTVSGFSLTNTAINMWRKP 60
Qy 61 GKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTAADTAVYCARGPPH 120
Db 61 GKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTAADTAVYCARGPPH 116
Qy 121 AMMRGVADYWGQGTIVTVSS 142
Db 117 -GTGTYGFEDYWGQGTIVTVSS 137

RESULT 2

US-08-943-136-4
Sequence 4, Application US/08943136
Patent No. 6291208
GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E
APPLICANT: Klein, Michel H
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,136
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-733
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-943-136-4

Query Match 73.5%; Score 545; DB 3; Length 140;

Best Local Similarity 76.2%; Pred. No. 1,1e-48;

Matches 109; Conservative 12; Mismatches 18; Indels 4; Gaps 2;

Qy 1 MAVLVFLCLVAFPPSC-VLSQVLOESGPGLVKPSQTLSTCTVSGFSLTSGVWVRP 59
Db 1 MALVLVFLSLAFAFPSCGVLSQVLOKESGPGLVAPSGSLITCTVSGFSLTSGVHWVRP 60
Qy 60 PGKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTAADTAVYCARGPP 119
Db 61 PGKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTAADTAVYCARGPP 120
Qy 120 HAMMRGVADYWGQGTIVTVSS 142
Db 117 -GTGTYGFEDYWGQGTIVTVSS 137

Db 121 DYV--HYAMDYWGQGTIVTVSS 140

RESULT 3

US-08-973-518-4
Sequence 4, Application US/08973518
Patent No. 6328962
GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E
APPLICANT: Klein, Michel H
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,518
FILING DATE: 07-APR-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-973-518-4

Query Match 73.5%; Score 545; DB 4; Length 140;

Best Local Similarity 76.2%; Pred. No. 1,1e-48;

Matches 109; Conservative 12; Mismatches 18; Indels 4; Gaps 2;

Qy 1 MAVLVFLCLVAFPPSC-VLSQVLOESGPGLVKPSQTLSTCTVSGFSLTSGVWVRP 59
Db 1 MALVLVFLSLAFAFPSCGVLSQVLOKESGPGLVAPSGSLITCTVSGFSLTSGVHWVRP 60
Qy 60 PGKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTAADTAVYCARGPP 119
Db 61 PGKGLLEMLGVINAGGTTNNYSALMSRLTISKDTSKNOVSLKLSVTAADTAVYCARGPP 120
Qy 120 HAMMRGVADYWGQGTIVTVSS 142
Db 121 DYV--HYAMDYWGQGTIVTVSS 140
RESULT 4
US-08-621-751A-4
Sequence 4, Application US/08621751A
Patent No. 5882644
GENERAL INFORMATION:
APPLICANT: Chang, Chung N.
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Martin, Ulrich
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR THE